

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 13, 2005, 16:04:47 ; Search time 831.561 Seconds  
(without alignments)  
4778.599 Million cell updates/sec

Title: US-10-062-879-2  
3412  
1 MAAGVAAWLPFAAAAGMM.....PGPNTNIPSTSVVXSVL 655

## Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5622541 segs, 303355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-DB=Published Applications NA -QPM=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Published Applications NA.\*  
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21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3412	100.0	2121	13	US-10-062-879-1
2	3300.5	96.7	2064	13	US-10-062-879-3
3	2498.5	73.2	2351	15	US-10-212-677-253
4	2498.5	73.2	2351	17	US-10-361-811-253
5	2498.5	73.2	2351	17	US-10-369-186-253
6	2498.5	73.2	2351	15	US-10-212-677-252
7	2498.5	73.2	5333	15	US-10-212-677-254
8	2498.5	73.2	5333	15	US-10-361-811-252
9	2498.5	73.2	5333	17	US-10-361-811-254
10	2498.5	73.2	5333	17	US-10-369-186-252
11	2498.5	73.2	5333	17	US-10-369-186-254
12	2104	61.7	3424	14	US-10-121-746-9
13	2070.5	60.7	2578	17	US-10-296-115-373
14	1658.5	48.6	5404	15	US-10-212-677-255
15	1658.5	48.6	5404	17	US-10-361-811-255
16	1658.5	48.6	5404	17	US-10-369-186-255
17	1490.5	43.7	1121	16	US-10-029-386-24777
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24	844	24.7	3254	17	US-10-369-186-251
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26	747	21.9	2565	17	US-10-435-935-10
27	747	21.9	3756	18	US-10-377-139-18
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43	715	21.0	2280	18	US-10-322-281-765
44	715	21.0	21587	18	US-10-322-281-91
45	715	21.0	22280	18	US-10-322-281-764

## ALIGNMENTS

RESULT 1  
US-10-062-879-1  
Publication No. US20020127649A1  
GENERAL INFORMATION:  
APPLICANT: Cockett, Mark I.  
APPLICANT: Dilks, Daniel W.  
APPLICANT: Chang Ling, Hual-Ping  
APPLICANT: Sokol, Patricia T.  
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
FILE REFERENCE: abd-98089  
CURRENT APPLICATION NUMBER: US/10/062, 879  
PRIOR APPLICATION NUMBER: 2002-01-31  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentm Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2121

TYPE: DNA  
ORGANISM: human  
US-10-062-879-1

## Alignment Scores:

Pred. No.:	0	Length:	2121
Score:	3412.00	Matches:	655
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	13	Gaps:	0

US-10-062-879-2 (1-655) x US-10-062-879-1 (1-2121)

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QY 21 ProValAlaAsnGlyProMetProLeuAlaProAlaAspLysAsnLysArgGlnAspGlu 40
Db CCGGTGGCCNAACGCGCCATGCGCCCGCCGCGCAAGAACAGCGGCAAGATGAG 192
QY 41 IleuIleValLeuAsnValSerGlyArgPheGlnThrTyrArgThrThrLeuGluArg 60
Db CTGATTCTCTCAACGAGTGGGCGGAGGTTCCAGACTCGAGAGACACGCTGAGCGC 252
QY 61 TyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThrLys 80
Db TACCGGACACCTCGTGGCGACACGAGAACAGAGTTCTTCAACAGAGACACCAAG 312
QY 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100
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QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200
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QY 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220
Db GTGGTGAAGACGGGCGCGTGGCGACGCTCCGCGACAGAGAGCTGCCGCGGAGG 732
QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240
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Db TACTCTCTGGGCGCTTCTGGGCGCTCCAGCGCGTACCGCTTACCGCAGCGTCAAGAG 852
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QY 281 AsnValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300
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QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340
Db CTGGGCTTCTTCTCTTCTTCTCCCTTCCATGCGCATCATCATCTTTGGCATTGAGTCTTT 1092
QY 341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTyrTyr 360
Db TATGCCGAGAGGGCTCTCGGCGCAGAGTTCACAGACATCCCTGCTGTTTGGTAC 1152
QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGly 380
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Db AACTTCTTCTCATACAGACAGATGTTGTCAAGTCTGTGCTTG 2037
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RESULT 2  
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 ; Sequence 3, Application US/10062879  
 ; Publication No. US20020127649A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cockett, Mark I.  
 ; APPLICANT: Dilks, Daniel W.  
 ; APPLICANT: Chang Ling, Hui-Ping  
 ; APPLICANT: Sokol, Patricia T.  
 ; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
 ; TITLE OF INVENTION: Polypeptides and Uses Therefor  
 ; FILE REFERENCE: amp-98089  
 ; CURRENT APPLICATION NUMBER: US/10/062, 879  
 ; CURRENT FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US/09/178,109  
 ; PRIOR FILING DATE: 1998-10-23  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2064  
 ; TYPE: DNA  
 ; ORGANISM: human  
 ; US-10-062-879-3

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 Score: 3300.50 Matches: 636  
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 Best Local Similarity: 97.10% Mismatches: 0  
 Query Match: 96.73% Indels: 19  
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US-10-062-879-2 (1-655) x US-10-062-879-3 (1-2064)

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 QY 221 ArgTyrSerValAlaPhePheCysLeuAAspThrAlaCysValMetIlePheThrValGlu 240  
 Db 733 CGTACTCGGTGGGCTTCTTGTGCTGCTGACACGGCGGTGCTCAAGATCTTCAACGTGGAG 792  
 QY 241 TyrLeuAenArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
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 QY 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
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 QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
 Db 913 GACGTGTCGGCGCTTCGTACAGCTCCGGGTTCGCGCTTCAAGATCTTCAAGTTT 972  
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 QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIysThrIleAlaGly 380  
 Db 1153 ACCATTGTCAACCAAGACACACTGGAGTACGAGAACATGGCTTAAGACATTCGAGG 1212  
 QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
 Db 1213 AAGATCTTGGCTCACTGCTGCTTGAAGGCGTCTGTGATTCCTGCGCTGCGTCTCT 1272  
 QY 401 ValIleValSerAenPheSerArgIleTyrHsGlnuAsnGlnuArgAlaAspLyAArgArg 420  
 Db 1273 GTGATTTGTTCCAACTTACCGGATTTTACCAACAGATACAGAGCTGATTAACGCAAG 1332  
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 Db 1333 GCACAAAAGAAAGCCCGCTTGGCAGGATCGTGTGCAAAACAGGACAGTTCAAAATGCA 1392  
 QY 441 TyrLeuHsSerIysAArgAsnGlyLeuLeuAsnGlnuAlaLeuGlnuLeuThrGlyThrPro 460  
 Db 1393 TACCTGACACAGCAAGCCCAACGGGCTCTCAACAGAGCGCTGAGCGGACCCCA 1452  
 QY 461 GluGlnuGlnuIleMetGlyLysThrThrSerLeuIleGluSerGlnuHsHsIleLeuLeu 480  
 Db 1453 GAAGAGAGACATAGGCGCAAGACCACTCATCTATGAGAGCCAGCATCATCACTGCTG 1512  
 QY 481 HisCysLeuGlnuIysThrThrGlyLeuSerTyrLeuValAspAspProLeuLeuSerVal 500  
 Db 1513 CACTGCTGGAATAAAACACCT----- 1533  
 QY 501 ArgThrSerThrIleuSaenHsGlnuPheIleAspGlnuGlnuMetPheGlnuAsnCys 520  
 Db 1534 -----AACCAAGATTTATGATAGCAAGATTTGAGCAAAATGTC 1575  
 QY 521 MetGluSerSerMetGlnuAenTyrProSerThrAArgSerProSerLeuSerSerHsPro 540  
 Db 1576 ATGAGAGATTCAATGAGAACTACCATCCACAAAGATCCCTCATGTCAGGACCA 1635  
 QY 541 GlyLeuThrThrThrCysCysSerArgArgSerIleLysThrThrHsIleuProAsnSer 560  
 Db 1636 GGCCTCACTACCACTGCTGCTCCCGTGAAGAAAGACCAACACCTGCCCAATTC 1695

QY 561 AsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHisIleGlnGly 580  
 Db 1696 AACCTGCACCTACTGCTCGCCGACGACATGCAAGACTGACGAGTTCACATCCAGGGGC 1755  
 QY 581 SerGlnGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAlaAspArg 600  
 Db 1756 AGTGAAGAGCCCTCTCTCAACACCATGCGTCCAGCTTATTTGAAACAGACAGCGAA 1815  
 QY 601 LeuArgProAsnGlySerThrSerGlnIleThrThrAlaIleIleSerIleProThrPro 620  
 Db 1816 CTGAGACCAAACTGCAAAACATCCAGATGACCAAGACCATCATCAGCATCCCTCC 1875  
 QY 621 ProAlaLeuThrProGlnGlyGluSerArgProProProAlaSerProGlyProAsnThr 640  
 Db 1876 CCAGCGCTAACCCCAAGGGGGAAGTGGCGCACCCCTGCGACGCCCAAGGCCCAACG 1935  
 QY 641 AsnIleProSerIleThrSerAsnValAlaValSerValLeu 655  
 Db 1936 AACATTCTTCCATTACCGACCAATGTTGTCAAGGTCTCTCTTGT 1980

RESULT 3  
 US-10-212-677-253  
 ; Sequence 253, Application US/10212677  
 ; Publication No. US20030129192A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chenault, Ruth A.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Harlocker, Susan J.  
 ; APPLICANT: McNeill, Patricia D.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.484C7  
 ; CURRENT APPLICATION NUMBER: US/10/212.677  
 ; CURRENT FILING DATE: 2002-08-02  
 ; NUMBER OF SEQ ID NOS: 288  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 253  
 ; LENGTH: 2351  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-212-677-253

Alignment Scores:  
 Pred. No.: 1,496-257 Length: 2351  
 Score: 2498.50 Matches: 486  
 Percent Similarity: 84.09% Conservative: 69  
 Best Local Similarity: 73.64% Mismatches: 70  
 Query Match: 73.23% Indels: 35  
 DB: 15 Gaps: 7

US-10-062-879-2 (1-655) x US-10-212-677-253 (1-2351)  
 QY 1 MetAlaIaGlyAlaValAlaIaIaTrrLeuProPheAlaArgAlaIaIaIleGlyTrrMet 20  
 Db 430 ATGGCGGGGGGGGGGAGGAGGTGGCTGCTTTGGCAAGGGGACGCGGTATCGGGGTGAATG 489  
 QY 21 ProValAlaAsnGlyPrrMetPrrLeuAlaProAlaAspLysAsnLysArg--GlnAsp 39  
 Db 490 CTTGTGGCTCTGGGGGCTTATGCGGGTCCCGGACGAGAGAGAGAGAGAGAGAGAGAGT 549  
 QY 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrrPargThrThrLeuGln 59  
 Db 550 GCTCTCATTTGGTGAATGTGAATGGACCGGCTTCCAGAGTGGGACGACACCTGGAA 609  
 QY 60 ArgGlyTrrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGlnLysPrr 79  
 Db 610 CGTAAACCAAGACCTTACTGGGCGAGTTCGAGAGGACTTTTCTTACCAACCAAGAACT 669  
 QY 80 LysGlnTrrPhePheAspArgAspProGlnValPheArgCysValLeuAsnPheTrrArg 99  
 Db 670 CAGCAGATTTTCTTGAACCGTGAACCAAGACATCTTCCGACCAATCTGAAATTTCTACCG 729

QY 100 ThrGlyLysLeuHisTrrProArgTrrGluCysIleSerAlaTrrAspAspGluLeuAla 119  
 Db 730 ACTGGAAGCTCCACTATCTCTGCCAGAGTGCATCTCTCTTACATGAAAGAACTGGCC 789  
 QY 120 PheTrrGlyIleLeuProGlnIleIleGlyAspCysTrrGlnGlnTrrLysAspArg 139  
 Db 790 TTTCTTGGCCCTCATCCGGAATCATCGGAGCTGCTTATGAGAGTACAAAGATCGC 849  
 QY 140 LysArgGluAsnAlaGluArgLeuMetCAspAspAsnAspSerGluAsnAsnGlnGluSer 159  
 Db 850 AGGAGAGAGAAACCGCGGCTGACAGACAGCGGATCCGACACCGCTGGGAGAGC 909  
 QY 160 --MetProSerLeuSerPheArgGlnThrMetTrrPargAlaPheGluAsnProHisTrr 178  
 Db 910 GCTTGCACCAATGACTGCGAGAGAGGTCTGAGGGGCTTCGAAACCCCAACACC 969  
 QY 179 SerThrLeuAlaLeuValPheTrrTrrValThrGlyPhePheIleAlaValSerValIle 198  
 Db 970 AGCAGATGGCCCTGGTGTCTTACTATGTACAGGGGTTTTCATTTGCGCTGTGTATC 1029  
 QY 199 ThrAsnValValGluThrValProCysGlyThrValProGlySer--LysGluLeuPro 217  
 Db 1030 GCGAATGTGTGAAGAAAGTCCGTCGAGATCAAGCCAGGTGACATTAAGAACTGCCC 1089  
 QY 218 CysGlyGlyArgTrrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db 1090 TGTGAAGCGGTAGTGTGTGGCTTCTTGTGTCGACAGGGCTGCGTCAAGATTTTC 1149  
 QY 238 ThrValGlnTrrLeuLeuArgPheAlaAlaProSerArgTrrArgPheIleArgSer 257  
 Db 1150 ACAGTGAGATTTTGTCTTGGCTGCGTGCAGCGCTGTAGTGTATCGTTTGTGGCGTAA 1209  
 QY 258 ValMetSerIleIleAspValValAlaIleMetProTrrTrrIleGlyLeuValMetThr 277  
 Db 1210 GTCATGAGTATCATGACGAGTGTGGCCATCTGCTTATTAACATTTGGCGTGAATACA 1269  
 QY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297  
 Db 1270 GACAAATGAGAGCGTACGAGGCTTTGTACACTCCAGATCTTCGGGTTCTCAGATC 1329  
 QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTrrThrLeuLysSerCys 317  
 Db 1330 TTTAAGTTTCCCGCACTCAAGGCTGCGCATCTCGGGGTACACATGAAGATGTGT 1389  
 QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
 Db 1390 GCTTCAGAAATGGGCTTCTTCTTCTCGCTACCAATGCTATCATCATCTTCGTACA 1449  
 QY 338 ValMetPheTrrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357  
 Db 1450 GTTATGTTCTACGAGAGAGGGGTCTTGGCTAGCAAGTTCAACAGCATCTCCGACGCC 1509  
 QY 358 PheTrrPrrThrIleValThrMetThrThrLeuGlyTrrGlyAspMetValProLysThr 377  
 Db 1510 TTCTGTATACATCTGATCATCATGACACTAAGGATGTGTGACATGTGGCCAAAC 1569  
 QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
 Db 1570 ATAGCAGGGAAGATTTTGTGTTATCTGTTCCGTAGAGGGGCTTGTGATGTCTTA 1629  
 QY 398 ProValProValIleValSerAsnPheSerArgIleTrrHisGlnAsnGlnAlaAsp 417  
 Db 1630 CTTGTTCCGGTGAATTTGATTCACATTCAGTGTCTTACCAACGAAATCAACGAGCAG 1689  
 QY 418 LysArgArgAlaGlnLysLysValArgLeuAlaArgIleArgValAlaLysThrGlySer 437  
 Db 1690 AAACAAAGGACCAAAAGAAAGCTTACAGTCCAGATCCGGGACGCCAAAGCGGAAC 1749  
 QY 438 SerAsnAlaTrrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnLysAlaGlnLeuThr 457  
 Db 1750 GCAATGTCTTACATGACAGCAAGCAAGGAAATGTTTACTAGTATCAAGCTGCAG--TCC 1806  
 QY 458 GlyThrProGlnGluGluHisMetCglyLysThrThrSerLeuIleGluSerGlnHisHis 477



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Db      1807 TCAGAGATGAGCAGGCTTTTGTAGCAAAATCCGGCTCCAGCTTTGAAACCAAGCAGCAC 1866
Qy      478 HistleuLeuHisCysleuGluIleThrThrGlyLeuSerTyrLeuValAspAspProleu 497
Db      1867 CACCTGCTTCACTGCTGGAAAAAACACG----- 1896
Qy      498 LeuSerValArgThrSerThrIleLysAsnHisgluPheIleAspGluIleMetPheGlu 517
Db      1897 -----AATCAGAGTTTGGAGCAGAACAGTCTTTGAA 1929
Qy      518 GluAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSer 537
Db      1930 GAAAGCTGATGAAAGTTGCAACTGTATATCGTCTTCAAGTACAGAGCTTCACTGCT 1989
Qy      538 SerHisProGlyLeuThrThrThrCysCysSerArgAspSerLysLysThrHisLeu 557
Db      1990 TCACAAAGAGGACACCAAGCAGCTGCTTTCAGCAGACCAAAAACTTTTCGCATC 2049
Qy      558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnIleLeuSerThrIleHis 577
Db      2050 CCAATGCTCAATGATATCAGGAAGCATATAGTATGATACAAAGAACTACAGACGATTCAG 2109
Qy      578 IleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLysAla 597
Db      2110 ATCAGATGTGTGAGAGAGAACCTCTGTCTAAAGCCGATCCAGTTTAAATGCCAAATG 2169
Qy      598 AspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrAlaIleIleSerIle 617
Db      2170 GAAAGTGTGTAAACTTAACCTGTAACAACTTATGATGACTACAGCAATATATAGCATC 2229
Qy      618 ProThrProProAlaLeuThrProGluGlyLeuSerArgPro-----ProProAlaSer 635
Db      2230 CCAATCACTCCAGTAACCAACCAAGAGAGAGAGATGAGCCAGAAATCCCTGAGTACTCA 2289
Qy      636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValIleValSerValIle 655
Db      2290 GGAAGG-----AATATTGTCAGAGTTTCTGCTTGG 2319

RESULT 4
US-10-361-811-253
; Sequence 253, Application US//10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-253

Alignment Scores:
Pred. No.: 1,49e-257 Length: 2351
Score: 2498.50 Matches: 486
Percent Similarity: 84.09% Conservative: 69
Best Local Similarity: 73.64% Mismatches: 70
Query Match: 17.23% Indels: 35
DB: 17 Gaps: 7

US-10-062-879-2 (1-655) x US-10-361-811-253 (1-2351)
Qy      1 MetAlaAlaGlyValAlaAlaIleTProleuProPheAlaAlaAlaIleGlyTyrMet 20
Db      430 ATGGCGGGGGGGTGGCAGCGTGGCTGCTTTTGGCAAGGCGAGCGGCTATCGGGGTGATG 489

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Qy      21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg--GlnAsp 39
Db      490 CCTGTGGCTCGGGGCTATGTCCGGCTCCCGAGGAGAGAGAGAAAGAACCAAGAT 549
Qy      40 GluLeuIleValIleAsnValSerGlyArgArgPheGlnThrThrPargThrLeuGlu 59
Db      550 GCTCTCATTTGGCTGAATGTGAGTGGGACCCGCTTCCAGACGTGGAGACACCTGTGAA 609
Qy      60 ArgTyrProAspThrLeuLeuGlySerThrGluLysgluPhePheAsnGluAspThr 79
Db      610 GATTACCAAGACACTTACTGGGAGATCTGAGAGGAGACTTTTCTACCAACCCAGAAACT 669
Qy      80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99
Db      670 CAGCAGATTCTTCTTGACCGGTGACCAAGCATCTTCCGCCACATCTGAATTTCTACCGC 729
Qy      100 ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119
Db      730 ACTGGAAAGCTCCACTCTCTCCGACAGAGTGCATCTCTGTACATGATGAAGAACTGGCC 789
Qy      120 PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArg 139
Db      790 TTCTTTGACCTCATCCGAAATATATCGGACTGCTGTATGAGAGTACAGAGATCGC 849
Qy      140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnLys 159
Db      850 AGCGGAGAGAAAGCGGAGCCCTGTCAGAGCAGCGGATACCGACACCGCTGGGAGAGC 909
Qy      160 --MetProSerLeuSerPheArgGlnThrMetTyrAlaPheGluAsnProHisThr 178
Db      910 GCCTTGCCCAACATGACTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 969
Qy      179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
Db      970 AGCAGATGGCCCTGGTGTCTACTATGTCAAGGAGTTTTCATGCGCTCTGTATC 1029
Qy      199 ThrAsnValAlaGluThrValProCysGlyThrValProGlySer--LysGluLeuPro 217
Db      1030 GCGAATGTGTGAGAAACATGTCCTCGTGGATCAAGCCAGGTCAATTAAAGAACTGCC 1089
Qy      218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db      1090 TGTGAGAGCGGTATGCTGTGCTTCTTCTGCTGTGACACGCGCTCGCATATATCTTC 1149
Qy      238 ThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257
Db      1150 ACAGTTAGATATTTGCTTCCCTGCTGCGTAGCGCTAGTGTTCACGTTTGTGCGTAGT 1209
Qy      258 ValMetSerIleIleAspValAlaIleMetProTyrTyrIleGlyLeuValMetThr 277
Db      1210 GTCATGATATCATCGACGTGTGTGCACTCTGCTTATTAACNTGGGCTGTGTATGACA 1269
Qy      278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
Db      1270 GACATGAGAGACGTCAAGGAGCTTTGTCACTCGAAGTCTCCGGGCTTTCAGAGATC 1329
Qy      298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317
Db      1330 TTTAAGTTTCCCGCCACTCTCAAGGCTCGCATCTCTGGGATACACACTGAAGAGTTGT 1389
Qy      318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
Db      1390 GCTTCAGAAATTTGGGCTTCTTGTCTTCTGCTCAACATGGCTATCATCATCTTGTGACA 1449
Qy      338 ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357
Db      1450 GTTATGTTTACGAGAGAGAGGAGGCTTTCGGCTAGCAAGTTTCAACAGACATCCCTGAGCC 1509
Qy      358 PheThrTyrThrIleValIleThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377
Db      1510 TTCTGTATTCACATCGTCAACATACACTAGGAGTATGTGATGATGTCGCAAAAACC 1569
Qy      378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397

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Db      1570 ATAGCAGGGAAGATTTTGGTTCATCTGTCGCTAGAGGAGTCTTGGATGCTCTTA 1629
Qy      398 ProValProValIleValSerAenPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417
Db      1630 CCGTTCGGGTGATGTGATTCACACTTCAGTCGATCTTACACACAGAAATACAGAGAGAC 1689
Qy      418 LysArgArgAlaGlnIlyValValAargLeuAlaArgIleArgValAlaIlyThrGlySer 437
Db      1690 AAACGAAGGGCACAAAAGAAAGTAGACTGGCCAGGATCCGGGACACCAAAAGCGGAGAC 1749
Qy      438 SerAsnAlaIleTyrLeuHisSerIlySerArgAsnGlyIleuLeuAsnGlnAlaLeuGluLeuThr 457
Db      1750 GCAAAATGCTTACATGCAGACCAAAACGAAATGTTTACTACATATACAGTCCAGCAG--TCC 1806
Qy      458 GlyThrProGlnGluGlnHisMetGlyIlyThrThrSerLeuIleGlnSerGlnHisHis 477
Db      1807 TCAGAGATAGACAGCGCTTTTGTAGCAAAATCCGGCTCCAGCTTTGAAACCCAGACACAC 1866
Qy      478 HisLeuLeuHisCysLeuGlnIlyValThrThrGlyLeuSerTyrLeuValAspAspProLeu 497
Db      1867 CACCTGCTTCACTGCTCGGAAAAAACACACG----- 1896
Qy      498 LeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGlnGlnMetPheGlu 517
Db      1897 -----AATCAGAGCTTGTGGACGAACAAGCTTTGAA 1929
Qy      518 GlnAsnCysMetGlnSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSer 537
Db      1930 GAAAGCTGCATGAGAGTGTGACACTGTTAAATCGTCTTCAAGTACAGCTCTTACAGTGT 1989
Qy      538 SerHisProGlyLeuThrThrThrCysCysSerArgArgSerIlyValThrThrHisLeu 557
Db      1990 TCACAACAAAGAGACACACACCTGCTTTCACGACGACACAAAACCTTTCCGAC 2049
Qy      558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHis 577
Db      2050 CCAAAATGCCAATGATATCAGAGAGCCATCAAGTATGATACAAAGCTCAGCAGATTCAG 2109
Qy      578 IleGlnIlySerGlnGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuIlyVal 597
Db      2110 ATCAGATGTGTGAGAGAAACACCTCTCTCTACAGCCGATCCAGTTAAATGCCAAAG 2169
Qy      598 AspAspGlyLeuArgProAsnCysIlyThrSerGlnIleThrThrAlaIleIleSerIle 617
Db      2170 GAAGAGTGTGTTAACTGAACCTGATGACCACTTATGTGACTACAGCAATATATACATC 2229
Qy      618 ProThrProProAlaLeuThrProGlnGlyGlnSerArgPro-----ProProAlaSer 635
Db      2230 CCAACACCTCCAGTACACACACCAAGAGAGAGATAGGCCAGAAATCCCTGAGTACTCA 2289
Qy      636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValIlyValSerValLeu 655
Db      2290 GGAGGA-----AATATGTGACAGGTTCTGCTTGG 2319

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RESULT 5  
US-10-369-186-253  
Sequence 253, Application US/10369186  
Publication No. US20030232056A1

GENERAL INFORMATION:  
APPLICANT: Fanger, Gary R.  
APPLICANT: Fling, Steven P.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.484C9  
CURRENT APPLICATION NUMBER: US/10/369,186  
CURRENT FILING DATE: 2003-02-14  
NUMBER OF SEQ ID NOS: 293  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 253  
LENGTH: 2351  
TYPE: DNA  
ORGANISM: Homo sapiens

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US-10-369-186-253
Alignment Scores:
Pred. No.: 1,49e-257 Length: 2351
Score: 2498.50 Matches: 486
Percent Similarity: 84.09% Conservative: 69
Best Local Similarity: 73.64% Mismatches: 70
Query Match: 73.23% Indels: 35
DB: 17 Gaps: 7

US-10-062-879-2 (1-655) x US-10-369-186-253 (1-2351)
Qy      1 MetAlaAlaGlyValAlaAlaATrPLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet 20
Db      430 ATGGCGCGCGGGGAGGAGCGCTGGCTCTTTTGGCAAGGGCAGAGCGCTATCGGGTGAATG 489
Qy      21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnIlySer---GlnAsp 39
Db      490 CCGTGGCTCGGGGCGCTATGCCGGCTCCCGCAGAGGAGAGAGAAAGAACCCAGAT 549
Qy      40 GlnLeuIleValIleAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59
Db      550 GCTCTCATTTGCTGAATGTGATGGGACCCGCTTCCAGACGTGGCAGACACCCCTGGAA 609
Qy      60 ArgTyrProAspThrThrLeuGlySerThrGlnIlyGluPhePheAsnGluAspThr 79
Db      610 GGTACCCAGACACTTACCTGGGCGAGTTCTGAGAGGACTTTTCTACACCCAGAAACT 669
Qy      80 LysGlnTyrPhePheAspArgAspProGlnValPheArgCysValIleAsnPheTyrArg 99
Db      670 CAGCAGTATTTCTTTGACCGGTGACCCAGACATCTTCCGCCACATCCGAAATTTCTACCG 729
Qy      100 ThrGlyLysLeuHisTyrProArgTyrGlnCysIleSerAlaTyrAspAspGlnLeuAla 119
Db      730 ACTGGAAAGCTCCACTATCTCCGACAGAGTCATCTCTGTTACGATGAAGAACTGGCC 789
Qy      120 PheTyrGlyIleLeuProGlnIleIleGlyAspCysCysTyrGlnGlyTyrIlyAspArg 139
Db      790 TTTCTTTGGCTTCATCCCGGAATATCATCGGACACTGCTGTATGAGAGTACAAAGATGCG 849
Qy      140 LysArgGlnAsnAlaGlnIlyArgLeuMetAspAspAsnAspSerGlnAsnAsnGlnIlySer 159
Db      850 AGCGAGAGAAACGCCGAGCGCTTCAGAGACGACCCGATACCCAGACCCGCGGGAGAGC 909
Qy      160 ---MetProSerLeuSerPheArgIleThrMetTrpArgAlaPheGlnAsnProHisThr 178
Db      910 GCCTTGCACCATGATCATGCAAGGACAGAGGCTCTGAGAGGCTTCGAGAACCCCCACACC 969
Qy      179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
Db      970 AGCAGATAGGCCCTGGTGTCTTACTATGTCAAGGGGTTTTTCATTTGCTCTGTATC 1029
Qy      199 ThrAsnValAlaGlnThrValProCysGlyThrValProGlySer---LysGlnLeuPro 217
Db      1030 GCGAATGTGGTGGAACAGTCCCTGGCGGATCAAGCCAGGTACATTAAGAATCTGCC 1089
Qy      218 CysGlyIlyArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db      1090 TGTGAGAGCGGTATGCTGTGGCTTCTTGTGTGACAGCGGCTCGTATGATCTTC 1149
Qy      238 ThrValGlnTyrIleuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257
Db      1150 ACAGTGTGATTTGGCTTGGCTGGCTGGACGGCTGAGCTGTAACCTTTTGTGCGTGAAT 1209
Qy      258 ValMetSerIleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThr 277
Db      1210 GTCATGAGTATCATGACGTGGTCCATCTGCTTATTTACATTTGGGCTGTATGACA 1269
Qy      278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
Db      1270 GACATAGAGAGAGTACGAGGAGGCTTTGTCACTCGAGTCTCCGGGCTTCAAGATC 1329
Qy      298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyIlyThrThrLeuLysSerCys 317

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Db 1566 GCGAATGTGTGGAAAACAGTCCGTCGATCAAGCCAGTCACTTAAAGACTGCC 1625  
 Qy 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db 1626 TGTGGAGAGCGGTATGCTGTGGCTTCTTCTGCTGTGACACGGCCGCTCATGATCTTC 1685  
 Qy 238 ThrValGluThrLeuLeuArgLeuPheAlaProSerArgTyrThrPheIleLeuAspSer 257  
 Db 1686 ACGATTGATATTGCTTCCCTGCTGACGCGCTGAGCTGATGCTTTCGTTGGCGTAT 1745  
 Qy 258 ValMetSerIleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
 Db 1746 GTCATAGATATCATCAAGCGTGGTGGCCATCTGCTTATTAATGCGCTGGGANTGACA 1805  
 Qy 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297  
 Db 1806 GACAAATGAGAGCGTCAGCGGAGCTTGTTCACACTCCGAGTCTCCGGGCTTCAGAGATC 1865  
 Qy 298 PheLeuPheSerArgIleSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317  
 Db 1866 TTTTAAGTTTCCGCCCACTTCAAGGCTGCGCATCTGGGATACACACTGAAAGATTGT 1925  
 Qy 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
 Db 1926 GCTCAGAAATGGGCTTCTTGTCTTCTGCTCAACATGCTATCATCTTCGCTACA 1985  
 Qy 338 ValMetPheTyrAlaGluArgIleSerSerAlaSerIlePheThrSerIleProAlaSer 357  
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 Qy 358 PheTyrTyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377  
 Db 2046 TTTCTGATACCATTCGTCACATGACAAACATAGGGATAGTGAATGGGCCAAAAC 2105  
 Qy 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
 Db 2106 ATAGCAGGAAAGATTTTGGTCTTATCTGCTTCCCTAGTGGGCTTGGCATGCTCTA 2165  
 Qy 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417  
 Db 2166 CTTGTCGGGTGATTGATCAACTTCAGTCGATCATCACACAGAAATCAACAGACAGAC 2225  
 Qy 418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrArgLysSer 437  
 Db 2226 AAACGAAAGGACAAAAGAAAGCTAGACGTGGCCAGATCCGGCACCCAAAACGGGAAC 2285  
 Qy 438 SerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
 Db 2286 GCAATGCTTACATGACGACGAAACGGAATGCTTACTCATGTAATCAGCTGCAG---TTC 2342  
 Qy 458 GlyThrProGluGluGlnHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477  
 Db 2343 TCAGAGATGACGAGCTTTTGTTAAGCAATCCGGGCTCCAGCTTGAACCCAGCACAC 2402  
 Qy 478 HisLeuLeuHisCysLysLeuGlyLysThrThrGlyLeuSerTyrLeuValAspAspProLeu 497  
 Db 2403 CACCTGCTTACATGCTCCGGAACCAACG--- 2432  
 Qy 498 LeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGlu 517  
 Db 2433 -----AATCAGAGATTGTTCAGCAACAGCTTTTGA 2465  
 Qy 518 GlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSer 537  
 Db 2466 GAAAGCGCATGAGAGTTGCAACTGTAATCGTCTTCAAGTCAAGTCTTCACTGCTCT 2525  
 Qy 538 SerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysLysThrThrHisLeu 557  
 Db 2526 TCACACACAGAGACACACACACCTGCTGTTCAGACACACAAAACCTTTTCCGATC 2585  
 Qy 558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnLeuLeuSerThrIleHis 577  
 Db 2586 CCAATGTCATATGATCAGAGAGCCATCAAGATGTAAGTAACAGAACTCAGACGATTCAG 2645

Qy 578 IleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAla 597  
 Db 2646 ATCAGATGTGTGAGAGAAACCTCTGTCTAACAGCGGATCCAGTTTAATGCCAAATG 2705  
 Qy 598 AspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleIleSerIle 617  
 Db 2706 GAAAGATGTGTAACTTAACCTGTAACCAACCTTAATGATCAACGAAATTAATAGCATC 2765  
 Qy 618 ProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAlaSer 635  
 Db 2766 CCAACACCTTCAGTAACACACACAGAGAGACGATGCGCAGAAATCCCTGAGTACTCA 2825  
 Qy 636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerValLeu 655  
 Db 2826 GAGAGA-----AATATTGTCAGAGTTTGTGCTTTG 2855  
 RESULT 7  
 US-10-212-677-254  
 ; Sequence 254, Application US/10212677  
 ; Publication No. US20030129192A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chenault, Ruth A.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: McNeill, Patricia D.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.484C7  
 ; CURRENT APPLICATION NUMBER: US/10/212.677  
 ; CURRENT FILING DATE: 2002-08-02  
 ; NUMBER OF SEQ ID NOS: 288  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 254  
 ; LENGTH: 5333  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-212-677-254  
 Alignment Scores:  
 Pred. No.: 5,81e-257 Length: 5333  
 Score: 2498.50 Matches: 486  
 Percent Similarity: 84.09% Conservative: 69  
 Best Local Similarity: 73.64% Mismatches: 70  
 Query Match: 73.23% Indels: 35  
 DB: 15 Gaps: 7  
 US-10-062-879-2 (1-655) x US-10-212-677-254 (1-5333)  
 Qy 1 MetAlaAlaGlyValAlaAlaIleTyrLeuProPheAlaArgAlaAlaIleGlyTyrPhe 20  
 Db 966 ATGGCGGGGGGGTGGACGCTGCTGCTTTGCAAGGGGACGCGCTATCGGGTGAATG 1025  
 Qy 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg---GlnAsp 39  
 Db 1026 CCTGAGGCTCGGGGCTTATGCGGCTCCCGGAGGACAGAGAGAAAGAACCCAAAGAT 1085  
 Qy 40 GluLeuIleValIleAsnValSerGlyArgArgPheGlnThrTyrArgThrThrLeuGlu 59  
 Db 1086 GCTCTCATTTGCTGAATGATAGTGGACCGGCTTCCAGAGCTGGACAGACACCTGGAA 1145  
 Qy 1146 CGTTACCCAGACACTCTACTGAGGAGTTCTGAGAGGAGCTTTTCTACACCCAGAAACT 1205  
 Qy 60 ArgTyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThr 79  
 Db 1206 CAGCATATTTCTTTGACCGGACCCAGACACATCTTCGCCACATCTGAAATTTTACCGC 1265  
 Qy 100 ThrGlyLysLeuHisTyrProArgTyrGlyCysIleSerAlaTyrAspAspGluLeuAla 119  
 Db 1266 ACTGGGAAGCTTCACTATCTCGCACAGATGCAATCTGCTTACATGAAGAACTGGCC 1325





Pred. No.:	5	81e-257	length:	5333
Score:	2498.50		Matches:	486
Percent Similarity:	84.09%		Conservative:	69
Best local Similarity:	73.64%		Mismatches:	70
Query Match:	73.23%		Indels:	35
DB:	17		Gaps:	7

US-10-062-879-2 (1-655) x US-10-361-811-254 (1-5333)

[illegible]

QY	318	AlAserGIuEnuGIyPheLeuLeuPheSerLeuThMeAlaLeilelePheAlAthr	337
Db	1926	GCCTCAGATTGGGCTTCCTGCTTCTCGCTCACATGGCTATCATCTTTCGCTACA	1985
QY	338	ValMePheTyAlaGIuLySGlySerSerAlaSerIysPheThrSerIleProAlaSer	357
Db	1986	GTTATGTTCTACGACGAGGAAGGGCTCTTCGGCTACGAAGTTCAACAGATCCCTGCAGCC	2045
QY	358	PheTPYrThrIleValThrMetThrThreugLyTyrgIyAspMetValProLyThr	377
Db	2046	TTCTGTATACCATCGTCACCATGACAACACTAGAGGTATGGTGTGATCGTCCAAAACC	2105
QY	378	IleAlaGIySleIlePheGlySerIleAcYSerLeuSerGlyValIleuValIleAlaLeu	397
Db	2106	ATACACAGGAGATATTTGGTTCTTATCTGTTCTGCTGAGTGGGGCTTGCTGATTCCTTA	2165
QY	398	ProValProValIleValSerAsnPheSerArgIleTyriSGlnAsnGlnArgAlaAsp	417
Db	2166	CTGTGTCGGATGTTGTTATTCCTCACTTCAGTCGATCTTACACACGAATCAACGAGCAGAC	2225
QY	418	LyAspArgAlaGlnLyLyAlaArgLeuAlaArgIleArgValAlaLyThrGlySer	437
Db	2226	AAACGAAGGGCAAAAAGAAAGTACAGCTGGCCAGATCCGGGACGCCAAAAGCGGAAGC	2285
QY	438	SerSernaIaTyrlLeuHisSerIyAspArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThr	457
Db	2286	CGAATATGCTTACACGACGAGCAAAACGGAATGGTTTACTCGAGTATACAGCTGGAC--TCC	2342
QY	458	GlyThrProGIuGIuGIuHisMetGlyLySerThrSerLeuIleGIuSerGlnHis	477
Db	2343	TCAGAGATGACGAGGCTTTGTGTACAAATCCGGCTCCAGCTTGAAACCCAGACACAC	2402
QY	478	HisLeuLeuHisCySleuGIuLySThrThrglyLeuSerTyrlLeuValAspAspProLeu	497
Db	2403	CACCTGCTTACCTCCGCAAAAAACACAG-----	2432
QY	498	LeuSerValaArgThrSerThrIleLyAsnHisGluPheIleAspGIuGlnMetPheGlu	517
Db	2493	-----AATCACAGATTTGGGACGAAACAAAGCTTTGAA	2465
QY	518	GlnAsnCyMetGIuSerSerMetGlnAsnTyProSerThrArgSerProSerLeuSer	537
Db	2466	GAAAGCTGCATGAGAAATTGCAACTGTATATCGTCTTCAAGTACAGCTTCACCTGCTCT	2525
QY	538	SerHisProGIuLeuThrThrThrCySleSerArgArgSerIySlyThrThrHisLeu	557
Db	2526	TCACACACAGAGATCACACGACACTGCTTTCACAGACACACAAAACCTTTCGCATC	2585
QY	558	ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnLeuSerThrIleHis	577
Db	2586	CCAAATGCGCAATGTATACGAAAGCATCAAGGTGTATACAAAGAACTCAGACACATTCAG	2645
QY	578	IleGlnGlySerGIuGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLyAla	597
Db	2646	ATCAGATGTGTGAGAGAAACACTCTGTCTTACAGCCGATCTCAAGTTTAAATGCCAAATVG	2705
QY	598	AspAspGIyLeuAspProAsnCySleThrSerGlnIleThrThrAlaIleIleSerIle	617
Db	2706	GAAAGATGTGTAAACCTTAACTGTGAAACACACTTATGTGACTACAGCAATAATAAGATC	2765
QY	618	ProThrProProAlaLeuThrProGIuGIuGluSerArgPro-----ProProAlaSer	635
Db	2766	CCAAACACTTCAGTAAACACACACGAGAGACATGAGGCCAGATCCCTCGAGTACTCA	2825
QY	636	ProGlyProAsnThrAsnIleProSerIleThrSerSernaValLySValSerValLeu	655
Db	2826	GAAGGA-----AATATTCGACAGATTTCGCTTGG	2855
RESULT 10			
US-10-369-186-252			
; Sequence 252, Application US/10369186			
; Publication No. US20030232056A1			
; GENERAL INFORMATION:			

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RESULT 10
US-10-369-186-252
; Sequence 252, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:

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Db	2706	GAAGAGTGTGTTAAACTTAACCTGTGAACAACCTTATGTGACTTACGACATATTAAGCATC	2765
Qy	618	ProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAlaSer	635
Db	2766	CCAACACTCCAGTATACCACACAGAAAGAGACGATAGCCAGATCCCTCGAGATCA	2825
Qy	636	ProGlyProAlaThrAsnIleProSerIleThrSerAlaValIleValSerValIleu	655
Db	2826	GGAGGA-----AAATATGTCAGAGTTTCGCTTGG	2855

```

RESULT 11
US-10-369-186-254
Sequence 254, Application US/10369186
Publication No. US20030232056A1
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF OVARIAN CANCER
FILE REFERENCE: 210121.484C9
CURRENT APPLICATION NUMBER: US/10/369,186
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 254
LENGTH: 5333
TYPE: DNA
ORGANISM: Homo sapiens
US-10-369-186-254

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Alignment Scores:	
Pred. No.:	5,81e-257
Score:	2498,50
Percent Similarity:	84,0%
Best Local Similarity:	73,6%
Query Match:	73,23%
DB:	17
	Gaps: 7
	Length: 5333
	Matches: 486
	Conservative: 69
	Mismatches: 70
	Indels: 35

US-10-062-879-2 (1-655) X US-10-369-186-254 (1-5333)

[illegible]

QY	160	---MetProSerLeuSerPheArgGlnThrMetTPArgAlaPheGlnAsnProHISThr	178
Db	1446	GCCTTGCCACCATGACTGCAAGGAGCGGCTGAGAGGCTTGAGAAACCCCAACACC	1501
QY	179	SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle	198
Db	1506	AGCAAGATGGCCCTGGTGTTCATGATGACAGGGGTTTTTCATGGCGGTCTGTGCATC	1561
QY	199	ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro	217
Db	1566	GCGAATGTGGTGAAGAACAGTCGCGCGATGCAACCCGAGTCACATTAAAGAACTGCC	1621
QY	218	CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe	237
Db	1626	TGTGGAGACCGGTATGCTGGCGCTTCTTGCTTGAGACAGGCTGCTCATGACTTTC	1681
QY	238	ThrValGluTyrLeuLeuArgLeuPheAlaIaProSerArgTyrArgPheIleArgSer	257
Db	1666	ACAGTTGAGTATTTGCTTCGCTGCGCTGAGCGCTTAAGTCGTTACCGTTTGTGCTAAT	1741
QY	258	ValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThr	277
Db	1746	GTCATGATATCATCATGACGTGGTGCCATCCGCTTATTCATTTGGGTGGATGACAC	1801
QY	278	AsnAsnGluAspValSerGlyValaPheValThrLeuAspValPheArgValaPheArgIle	297
Db	1806	GACATGAGGACGTCACGCGAGCCCTTGTCAACCTCCAGTCCTCCGGGTCTTCAGGATC	1861
QY	298	PheIysPheSerArgHISerGlnGlyLeuArgIleLeuGlyTyrThrLeuIysSerCys	317
Db	1866	TTTAAAGTTTCCCGCAGCTCTCAAGGCTCGGCGATCTGGGGGTACACATGAAGATTGT	1921
QY	318	AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr	337
Db	1926	GCCTCAGATTGGGCTTCTGCTTTCTTCGCTCACCACATGCGTATCATCATCTTCGCTACA	1981
QY	338	ValMetPheTyrAlaGluIysGlySerSerAlaSerIysPheThrSerIleProAlaSer	357
Db	1986	GTTATGTCTTCAGCAGAAAGGGGCTTCCGCTGACCAAGTTCACACAGCATCCCTCGACGC	2041
QY	358	PheTyrPyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIysThr	377
Db	2046	TTCTGGATACCATGTCATGCAACATGACAACTAGGGTATGGAGCATGGTGCAAAACCC	2101
QY	378	IleAlaGlyIysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu	397
Db	2106	ATTAGCAGGAAGATTTTGGTCTCATCTGTTCCGTGCGTAGTGGGGTCTTGGTCACTGCTCA	2161
QY	398	ProValProValIleValSerAsnPheSerArgIleTyrHISGlnAsnGlnArgAlaAsp	417
Db	2166	CCTGTTCGGGTATGTATCCAACTTGACGTGCATCTACACAGATATCAAGACAGAC	2221
QY	418	LysArgArgAlaGlnIysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer	437
Db	2226	AAACGAAAGGCAAAAGAAAGCTAAGATGCGCAGATGCCGGGCGCCAAAGCGGAAC	2281
QY	438	SerAsnAlaTyrLeuLeuHISerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThr	457
Db	2286	GCAATGTCTTACATGACAGCAAAACGGATGGTTTATCTCAGTATACGCTGACG---TCC	2341
QY	458	GlyThrProGlnGluGlnHISerMetGlyLysThrThrSerLeuIleGluSerGlnHISerHIS	477
Db	2343	TCAAGAGATGACAGAGGCTTTTGTTAAGCAAAATCCGGCTCAGCTTTGAAACCAAGCACAC	2401
QY	478	HISLeuLeuHISerCysValLeuGluLysThrThrGlyLeuSerTyrLeuValaAspAspProLeu	497
Db	2403	CACCTGTCTTCACTGCTGGAAAAAACCCG-----	2431
QY	498	LeuSerValaLysThrSerThrIleLysAsnHISGluPheIleAspGluGlnMetPheGlu	517
Db	2433	-----AATCACAAGTTTGTGGACCAACACAGTCTTTGAA	2461
QY	518	GlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSer	537

Db 2466 GAAAGCTGATGAGTGTGAACTGTAAATCGCTTCAAGTCACAGTCTTCACTGCT 2525  
Qy 538 SerHisProGlyLeuThrThrThrCysSerArgArgSerIleYerThrHisLeu 557  
Db 2526 TCACAAAGAGAGTCAACGACACTGCTGTTCACGACGACAAAACCTTTGGCAGTC 2585  
Qy 558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGlnLeuSerThrIleHis 577  
Db 2586 CCAAAATGCCAATGTATCAGAGACCCATCAAGGTAGTATCAAGAACTCCGACGATTCAG 2645  
Qy 578 IleGlnGlySerGlnGlnProSerLeuThrThrThrSerArgSerSerLeuAsnLeuVal 597  
Db 2646 ATGAGATGTGTGAGAGAACACCTGTGTCTAACAGCCGATCCAGTTAAATGCCAAATG 2705  
Qy 598 AspAspGlyLeuArgProAsnCysIleThrSerGlnIleThrThrAlaIleIleSerIle 617  
Db 2706 GAAGAGTGTCTTAACCTAACTGTGAACAACCTTATGTGACTACAGCAATATTAAGCAGTC 2765  
Qy 618 ProThrProProAlaLeuThrProGlnGlyGlnSerArgPro----ProProAlaSer 635  
Db 2766 CCAACACCTCCAGTAAACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2825  
Qy 636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValValIleValSerValIle 655  
Db 2826 GGAGGA-----AATATTGTCAAGATTCTGCTTG 2855

RESULT 12  
US-10-121-746-9  
Sequence 9, Application US/10121746  
Publication No. US20030036648A1  
GENERAL INFORMATION:  
APPLICANT: Muller, Andrew P.  
APPLICANT: Curran, Mark Edward  
APPLICANT: Hu, Ping  
APPLICANT: Ruter, Marc  
APPLICANT: Wang, Jian-Wang  
TITLE OF INVENTION: No. US20030036648A1 Human Potassium Channels  
FILE REFERENCE: SEQ-15P  
CURRENT APPLICATION NUMBER: US/10/121,746  
PRIORITY FILING DATE: 2002-04-11  
PRIORITY APPLICATION NUMBER: US/09/336,643A  
PRIORITY FILING DATE: 1999-06-18  
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687  
PRIORITY FILING DATE: EARLIER FILING DATE: 1998-08-07  
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448  
PRIORITY FILING DATE: EARLIER FILING DATE: 1999-01-19  
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826  
PRIORITY FILING DATE: EARLIER FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 3424  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (257)...(2195)  
OTHER INFORMATION: K+hov12  
US-10-121-746-9

Alignment Scores:  
Pred. No.: 7,77e-215 Length: 3424  
Score: 2104.00 Matches: 429  
Percent Similarity: 74.78% Conservative: 78  
Best Local Similarity: 63.27% Mismatches: 117  
Query Match: 61.66% Indels: 54  
DB: 14 Gaps: 14

US-10-062-879-2 (1-655) x US-10-121-746-9 (1-3424)

Qy 1 MetAlaAlaGlyValAlaAlaAlaTProLeuProPheAlaArgAlaAlaAlaIleGlyTTPMc 20  
|||||  
|||||

Db 257 ATGGCGGAGAGCCCTGGCAGCTGCTGCTTTTGTCTCGGGCAGACAGAGTGGGCTGCTG 316  
Qy 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspIleValSerGlnIleVal 40  
Db 317 CCCCCGGCCAGCAACCCCTGCCCCCGGACCCGGGGGTGAAGCCATCTCAGAGAGATGG 376  
Qy 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnIleThrPheArgThrIleValArg 60  
Db 377 GTTCTGTGTGTGAACGTGACGAGCGGGCTTTGAGCTTGGAAGAAATACGTGACCGC 436  
Qy 61 TyrProAspThrLeuLeuGlySerThrGlnIleGlyIlePhePheAsnGlnIleAspThrIle 80  
Db 437 TACCAAGACACCTTCTGGGAGCTCGGAGAGAGAAATCTTCTACAGATGCTGACAGC 496  
Qy 81 GlnTyrPhePheAspArgProGlnValPheArgCysValLeuAsnPheTyrArgThr 100  
Db 497 GAGTACTTCTTCATCCGACCTGACATGTCGCGCATGTGCTGAAGCTTCAACCGAAG 556  
Qy 101 GlyIleLeuHisTyrProArgTyrGlnCysGlnSerIleTyrAspAspGlnIleValPhe 120  
Db 557 GGGGGGCTGATTCGCCAGCGCAGAGAGAGATGATCCAGGCTTCAGACGAAGCTGCTTTC 616  
Qy 121 TyrGlyIleLeuProGlnIleIleGlyAspCysTyrGlnGlnTyrIleAspArgIle 140  
Db 617 TACGGCTCGTCCCGAGCTAGTGTGATGCTGCTGCTTGAAGATACGGAGCCGAAG 676  
Qy 141 ArgGlnAlaAlaGlyArgLeuMetAspAspAsnAspSerGlnIleValSerMet 160  
Db 677 AAGAGAAATGCCGAGCCCTGCGCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 723  
Qy 161 ProSerLeu-----SerPheArgGlnThrMetThrPheArgAlaPheGlnAspPro 176  
Db 734 CCAGCCCTGCGCAGAGAGAGCTCTCGGAGAGGCTGCGGAGGCTTCGAGAAATCCA 793  
Qy 177 HisThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSer 196  
Db 794 CACAGAGACCGGAGAGCCCTGCTTTCTACTATGTGACCGGCTTCTCATGCGGCTCG 853  
Qy 197 ValIleThrAsnValValGlnThrValProCys-----GlyThrValProGlySerIle 214  
Db 854 GTCATCGCCATGTGTGTGAGACCATCCATGCGCGGCTCTGACCGCAGGCTCTCAAG 913  
Qy 215 GlnLeuProCysGlyIleValGlyTyrSerValAlaPhePheCysLeuAspThrAlaCysVal 234  
Db 914 GAGAGCCCTGTGGCAGAACGCTTCCACAGGCTTTTTCAGAGACAGAGCCTGTGTA 973  
Qy 235 MetIlePheThrValGlyTyrIleLeuArgLeuPheAlaIleAspSerArgTyrArgPhe 254  
Db 974 CTCATATTCAAGGTGANTACTCTCGGCTGTTTCCGCCCCAGCCGTTGCCGCTTC 1033  
Qy 255 IleArgSerValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeu 274  
Db 1034 CTGGGAGATGTCAAGAGCTCATGAGTGTGAGTGTGCGCTTCCCTTCAATTGAGGCTT 1093  
Qy 275 ValMetThrAsnAsnGlnAspValSerGlyAlaPheValThrLeuAlaValPheArgVal 294  
Db 1094 TTGGTCCCAAGAACGAGATGTCTGGGCTTTCATCCCTGCGGTGTTCCGGGTG 1153  
Qy 295 PheArgIlePheIlePheIlePheSerArgHisSerGlnIleLeuArgIleLeuGlyTyrThrLeu 314  
Db 1154 TTTGCACTTTCAGATTTCTCAGGCACTCAGAGGCTTTAGAGATTCTGGGCTACACATC 1213  
Qy 315 LysSerCysAlaSerGlnLeuGlyIlePheLeuLeuPheSerLeuThrMetAlaIleIle 334  
Db 1214 AAGAGCTGTGCTGAGCTGGCTTCTCTCTTTCCCTTAAACATGAGCATCATCATC 1273  
Qy 335 PheAlaThrValMetPheTyrAlaGlyIleSerGlnIleAspThrIleSerIle 354  
Db 1274 TTTGCACTTTCAGATTTTATGCTGAGAGGCAACAAACAGACCACTTTCAGAGATC 1333  
Qy 355 ProIleSerPheTyrTyrThrIleValThrMetThrThrLeuGlyTyrArgIleAspMetVal 374  
Db 1334 CTTGGGCTTGTGTATACATTGTCACTGACCAAGCTTGGCTTGGAGACATGTG 1393

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QY 375 ProlyserThrIleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuVal 394
DB 1394 CCCAGCACACATGGCTGGAGAAATTTTGGCTCCATCGCTACAGTGGGGCTTGGTTC 1453
QY 395 IleAlaLeuProValProValIleValSerAsnProSerArgIleTyrHISGlnAsnGln 414
DB 1454 ATTGCCCTGGCTGGCCAGTATGTGTCCAACTTTCAGCCGCACTACACAGAACAG 1513
QY 415 ArgAlaAspLysArgValGlnIleLysLysAlaArgLeuAlaArgIleArgValAlaLys 434
DB 1514 CGGGCTCAACAGCCGCCAGCAGACAGAGAGTGGCTTGGAGAGATCCGATTGGCAAG 1573
QY 435 ThrGlySerSerAsnAlaTyrLeuHISerLysArgAsnGlyLeuLeuAsnGlnAlaLeu 454
DB 1574 AGTGTATCCACCAATGGCTTCTTCAGTACAGAGAAATGGG-----GGCCTT 1621
QY 455 GluLeuThrGlyThrProGluGluGlnHISerMet-----GlySerThrSerLeuIleGlu 473
DB 1622 GAGGACAGCGGCACTGGCGAGGAACAGGCTCTTGTGTACAGAACCCGTTCCGCTTGA 1681
QY 474 SerGlnHISerLysIleLeuLeuHISerLeuGluLysThrThrGlyLeuSerTyrLeuVal 493
DB 1682 CAGCAACATCAACCACTTGTGCTGCACTGTAGAGAAACAAG----- 1723
QY 494 AsparProLeuLeuSerValArgThrSerThrIleLysAsnHISGluPheIleAspGlu 513
DB 1724 -----TCCATGAGTTACAGATGAG 1744
QY 514 GlnMetPheGluGlnAsnCysMetGlySerSerMetGlnAsnTyrProSerThrArgSer 533
DB 1745 CTCACCTTCACTGA---GCCCTGGAGCCCTTCGCCGGTGGCCGACCAAGCCGTTAGC 1801
QY 534 ProSerLeuSerSerHISPro-----GlyLeuThrThrThrCysCysSerArg 549
DB 1802 ACCCTGTGTCTTCCAGCCAGTGGAGACCCGGAAGCTGTCTCTTGTCTGCCCTTGC 1861
QY 550 ArgSerLys--LysThrThrHISerLeuProAsnSerAsnLeuProAlaThrArgLeuArg 568
DB 1862 AGGGCAAGCGCCGCGCATCCGCTTGGCCAACTCCACTGCTCAGTCAAGCCG---GAC 1918
QY 569 SerMetGlnGluLeuSerThrIleHISIleGlnGlySerGluGlnProSerLeuThrThr 588
DB 1919 AGCATGACAGAGCTGGACATG-----CTGGCAGGGCTGGCCAGAGACCATGCCCTCAG 1972
QY 589 SerArgSerSerLeuAsnLeuLysAlaAspAspGlyLeuArgProAsnCysLysThrSer 608
DB 1973 AGCGGCTCCAGCCTCAATGCCAAGCCCATGACAGCTTACCTGAAGTGGAGACCGCG 2032
QY 609 GlnIleThrThrAlaIleIleSerIleProThrProProAlaLeuThrProGluGlyGlu 628
DB 2033 GACTTCGTGGCTGCATTAATCAGATCCCTAACCCCTCGCCAAACCCCGAGT---GAG 2089
QY 629 SerArgProProProAlaSerProGly----- 637
DB 2090 AGCCAA-----CCTTCTCTCCCTGGCGCGGTGGCAGGCGCCGAGACCCCTCAGAAC 2143
QY 638 ProAsnThrAsnIleIleSerIleThrSerAsnValValLysValSerValLeu 655
DB 2144 TCCAGCTGGGTACCCCTTGGCTTCCCGCAGACGTGCAGATCTATCCCTG 2197

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RESULT 13
US-10-296-115-373
; Sequence 373, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIORITY FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21

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; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 373
; LENGTH: 2578
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-373

Alignment Scores:
Pred. No.: 1,95e-211 Length: 2578
Score: 2070.50 Matches: 426
Percent Similarity: 75.00% Conservative: 84
Best Local Similarity: 62.65% Mismatches: 115
Query Match: 60.68% Indels: 56
DB: 17 Gaps: 14

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US-10-062-879-2 (1-655) x US-10-296-115-373 (1-2578)

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QY 1 MetAlaAlaGlyValAlaIleAlaThrLeuProPheAlaArgAlaAlaIleGlyTyrMet 20
DB 1 ATGGCGGCAAGGCTGGCCAGCTGCTGCTTTCCTGGGCAAGAGATCTCGAGAGATGAG 60
QY 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArgGlnAspGlu 40
DB 61 CCCCTGGCCAGCAACCCCTGCCCGCCGCAACCGGGGGTGAAGCATCTCGAGAGATGAG 120
QY 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrThrArgThrThrLeuGluArg 60
DB 121 GTTCTGTGTGTGAACCTGAGCGAGCGGCGCTTTCGAGCTTGAAGATACGCTGGACCGC 180
QY 61 TyrProAspThrLeuLeuGlySerThrGlyLysGluPhePheAsnGluAspThrLys 80
DB 181 TACCAACACACCTTGTGGGAGCTCGAGAGAGAAATCTTTCAGATGCTGACTCAGGC 240
QY 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100
DB 241 GAGTACTTCTTCATCCGACACCTGACATGTTCCGCAATGTCGTAACCTTACCGAAGC 300
QY 241 GlyLysLeuHISerTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120
DB 301 GGGGCGGTGATGCGCCAGCGAGAGATGATCAGGCTTTCAGAAAGCTGGCTTTC 360
QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysSerTyrGluTyrLysAspArgLys 140
DB 361 TACGCTGTGTCCCGAGCTAGTGGTGTGCTGCTTGAAGAGTATCGGAGCGAAG 420
QY 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnSerGlnAsnGlnGlnSerMet 160
DB 421 AAGAGAAATCCAGACCCCTGGCAGAGATGAGAGGACAGACGCGCGGAGCGC--- 477
QY 161 ProSerLeu-----SerPheArgGlnThrMetTyrPargAlaPheGluAsnPro 176
DB 478 CCAACCTCGCAGAGAGCAGACTCCCTCGGCGAGGCGCTTGGCGGCGCTTCGAGAAATCCA 537
QY 177 HisThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSer 196
DB 538 CACACGAGCACCGGAGCCCTGTTTCTACTATGTGACGAGCTTTCATCGCCGTGTG 597
QY 197 ValIleThrAsnValValGluThrValProCys-----GlyThrValProGlySerLys 214
DB 598 GTCATGCCAATGTGTGGAGACCATCCATGCCGCGCTCTGAGCCAGCATCTCTCAAG 657
QY 215 GluLeuProCysGlyArgTyrSerValAlaPhePheCysLeuAspThrAlaCysVal 234
DB 658 GAGCAGCCCTGTGGCGAAGCTTCCACAGAGCTTTCATGACAGACGCTGTGTA 717
QY 235 MetIlePheThrValGluTyrLeuLeuArgLeuPheAlaIleProSerArgTyrArgPhe 254
DB 718 CTCATATTCAGAGTGAATCTCTCCGCTGTGTTCGCGCCGACCGCTTGCCTTC 777
QY 255 IleArgSerValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeu 274

```

Db 778 CTGGAGTGTGATGAGCTCATGACGTGTGGCCATCTGCTTACTTACATGAGGCTT 837  
Qy 275 ValMetThrAsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgVal 294  
Db 838 TTGTGCCCCAAGACGATGTCCTGTGGGCTTTGTGACCTGTGTGTGTCCGGGGT 897  
Qy 295 PheArgIlePheIlePheSerArgHisSerGlnGlyLeuArgIleLeuGlyIleThrLeu 314  
Db 898 TTTCGATCTTCAAGTTCTTCAGGCACTACAGGGCTTGAAGATTCTGGGCTACACACTC 957  
Qy 315 LysSerCysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIle 334  
Db 958 AAGAGGTGTGCTGTGAGCTGGGCTTCTCTCTTCCCTTACATGAGCATCATCATC 1017  
Qy 335 PheAlaThrValMetPheIleIleGlyIleGlySerSerAlaSerIlePheThrSerIle 354  
Db 1018 TTGTCCACTGTCTCATGTTTATGCTGAGAGGGCAAAACCAACCTTTCACAGCATC 1077  
Qy 355 ProAlaSerPheIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 374  
Db 1078 CTTGGGCTTCTGTGTATACATTTGTCACATGACCAAGCTTGGCTACGAGACATGTG 1137  
Qy 375 ProIleThrIleAlaGlyIlePheGlySerIleCysSerLeuSerGlyValLeuVal 394  
Db 1138 CCGAGACCATTTCTGGCAAGATTTTCGGGTCCATGCTGCTCATGAGGCGTCTTGTG 1197  
Qy 395 IleAlaLeuProValProValIleValSerAsnPheSerArgIleIleIleGlnGln 414  
Db 1198 ATTGGCTGCTGTGCGAGCATGTTGTCCACTTTAGCGCGCATTCACCAACCAAGCAG 1257  
Qy 415 ArgAlaAspLysArgArgAlaGlyIleIleIleIleIleIleIleIleIleIleIleIle 434  
Db 1258 CGGAGCTGACAGGCGGAGACAGAGAGGTGCGCTTGGCAAGATTCGATTTGGCAAG 1317  
Qy 435 ThrGlySerSerAsnAlaIleIleIleIleIleIleIleIleIleIleIleIleIle 454  
Db 1318 AGGTGTACACCAATGCTTCTGTGACATGACAGACAGATGGG-----GGCTTT 1365  
Qy 455 GluLeuThrGlyThrProGluGluGluIleMet--GlyLysThrThrSerLeuIleGlu 473  
Db 1366 GAGACACGCGCGAGTGGCGAGAAACAGCTGTTGTGTGTCAGAAACGCTTGTGTA 1425  
Qy 474 SerGlnHisHisIleLeuHisIleCysLeuGluIleThrThrIleIleIleVal 493  
Db 1426 CAGCAATACCACTTGTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1467  
Qy 494 AspAspProLeuLeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGlu 513  
Db 1468 -----TGCATAGATTCAAGATGAG 1488  
Qy 514 GluMetPheGluGluAsnCysMetGluSerSerMetGlnAsnIleProSerThrArgSer 533  
Db 1489 CTCACCTTCAAGTAA--GCCCTGGAGCGCTCTGCGCGGTTGCGCGCACCAACCTTAC 1545  
Qy 534 ProSerLeuSerSerHisPro-----GlyLeuThrThrThrCysCysSerArg 549  
Db 1546 ACCCTGTGTCTTCCACGACGAGTGGACCCGAAAGCTGTGCTTCTTGTGCTGCTGCTG 1605  
Qy 550 ArgSerLys--LysThrThrHisLeuProAsnSerAsnLeuProAlaThrArgLeuArg 568  
Db 1606 AGGGCCAAAGCGCGCGCATCCGCTTGGCACTCCA--CTGCTCAGTACGCGGTGGGA 1663  
Qy 569 SerMetGlnGluLeuSerThrIleHisIleGlnGly--SerGluGlnProSerLeuThr 587  
Db 1664 GGCATGACGAGAGCTGACATG-----CTGACAGGGCTTGCAGAGGAGCATCCCTTC 1717  
Qy 588 ThrSerArgSerSerLeuAsnLeuValAlaAspArgIleLeuArgProAsnCysLysThr 607  
Db 1718 AGAGCCGCTCAGCTTCAATGCCAAGCCCATGACGCTTGAACCTGACAGCAGCAG 1777  
Qy 608 -SerGlnIleThrThrAlaIleIleIleIleIleIleIleIleIleIleIleIleIle 627  
Db 1778 GGGGAGCTTGTGTGCTGCTGCTTATACAGATCCCTACCTCTGCGCAACCCCAAGAT-- 1835

Qy 627 yGluSerArgProProAlaSerProGly----- 637  
Db 1836 -GAGAGGCCAA-----CTTCTCTCCCTGGGCGGTGGAGCGCGGACACCTCAG 1888  
Qy 638 ----ProAsnThrAsnIleProSerIleThrSerAsnValValIleValSerValLeu 655  
Db 1889 GAACCTCCAGCCTGGGTACCCCTTGTCTTCCCGGACAGCTGCAAGATCTCATCCCTG 1946  
RESULT 14  
US-10-212-677-255  
; Sequence 255, Application US/10212677  
; Publication No. US20030129192A1  
; GENERAL INFORMATION:  
; APPLICANT: Chemault, Ruth A.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.4847  
; CURRENT APPLICATION NUMBER: US/10/212.677  
; CURRENT FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 288  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 255  
; LENGTH: 5404  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-677-255  
Alignment Scores:  
Pred. No.: 1,42e-166 Length: 5404  
Score: 1658.50 Matches: 320  
Percent Similarity: 87.71% Conservative: 37  
Best Local Similarity: 78.62% Mismatches: 33  
Query Match: 48.61% Indels: 17  
Gaps: 5  
US-10-062-879-2 (1-655) x US-10-212-677-255 (1-5404)  
Qy 1 MetAlaIleGlyValAlaAlaIlePheProPheAlaIleAlaIleGlyTrpMet 20  
Db 1369 ATGGCGCGCGGGGTGGAGCTGTGCTTGTGCAAGGCGGCGCTATCGGGTGAATG 1428  
Qy 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnIleArg--GlnAsp 39  
Db 1429 COTGTGGCTGCGGGGCTATGCTGCGCTCCCGGAGGACAGAGAGAGAAAGCAACCAAGAT 1488  
Qy 40 GluLeuIleValIleAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59  
Db 1489 GCTTCATATGTGTGAGATGTAAGTGGACCCGCTTCCAGACGTGGGACACACCTTGA 1548  
Qy 60 ArgTrpProAspThrLeuLeuGlySerThrGluIleGluPhePheAsnGluAspThr 79  
Db 1549 CGTACCCAGACCTTCTTGAACCGTGAACCAAGACATCTTCCGCCACATCGTAATTTCTAC 1608  
Qy 80 LysGluTrpPhePheAspArgAspProGluValPheArgCysValIleAsnIlePheTrpArg 99  
Db 1609 CAGCAGATTTCTTGTGACCGTGAACCAAGACATCTTCCGCCACATCGTAATTTCTAC 1668  
Qy 100 ThrGlyLysLeuHisIleTrpProArgTrpGluCysIleSerAlaIleAspAspGluLeuAla 119  
Db 1669 ACTGGGAAGCTCCACTATCTCTGCGACAGAGTGCATCTCTGCTTACGATGAAGAACTG 1728  
Qy 120 PheTrpGlyIleLeuProGluIleIleGlyLysProCysTrpGluIleIleIleIleIle 139  
Db 1729 TTCTTGTGCTCATCTCCGAAATCATGCGGCACTGCTGTATGAGAGTACAAAGATGCG 1788  
Qy 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSer 159  
Db 1789 AGCGAGAGAAACCGGAGCGCTCTGACAGACACCGCATACCAACACCGCTGGGAGAGAGC 1848



```

QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
| | | | |
Db 2329 GCCTCAGAAATGGGCTTCTTGTCTTCTGCTCACCATGGCTATCATCTTCCCTCA 2388
| | | | |
QY 338 ValMetPheThrAlaGluLeuGlySerSerAlaSerIlePheThrSerIleProAlaSer 357
| | | | |
Db 2389 GTTATGTTCTACCGCAAGAAAGGGGCTTCGGCTAGCAAGTTCCACGACATCCCTGAGCC 2448
| | | | |
QY 358 PheTrpTyrrThrIleValThrMetThrThr-----ProLeuThrIleAlaGlyIlePhe 367
| | | | |
Db 2449 TTCTGTATATACCATCTGCTCACCATGACACCACTAGGCTAGTCCCATTAATGGAAATGGGA 2508
| | | | |
QY 368 -----LeuGlyTyrrGlyAspMetVal-----ProLeuThrIleAlaGlyIlePhe 383
| | | | |
Db 2509 TGGAGGTGGGTATGGGTAGCGCATTTGACCCCATCGAGTTACATGTAATCCGGG 2568
| | | | |
QY 384 GlySerIleCySerLeuSer 390
| | | | |
Db 2569 GAAATCATTTGTTTCTTCTCC 2589
| | | | |

```

## RESULT 16

```

US-10-369-186-255
; Sequence 255, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 5104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-255

```

## Alignment Scores:

```

Pred. No.: 1.42e-166 Length: 5404
Score: 1658.50 Matches: 320
Percent Similarity: 87.71% Conservative: 33
Best Local Similarity: 78.62% Mismatches: 33
Query Match: 48.61% Indels: 17
DB: 17 Gaps: 5

```

US-10-062-879-2 (1-655) x US-10-369-186-255 (1-5404)

```

QY 1 MetAlaAlaGlyValAlaAlaATPLeuProPheAlaArgAlaAlaIleGlyTrpMet 20
| | | | |
Db 1369 ATGGCGGGGGGGGTGGCGAGCTGGCTGCTTTGGCAAGGGCAGCGCTATCGGTGAGAG 1428
| | | | |
QY 21 ProValAlaAaAaCysProMetProLeuAlaProAlaAspIleAsnIleArg---GlnAsp 39
| | | | |
Db 1429 CCGTGGCTCGCGGCTATGCGGCTCCCGCAGGAGAGAGAGAAAGAACCCAGAT 1488
| | | | |
QY 40 GluLeuIleValLeuAaAaValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59
| | | | |
Db 1489 GCTCTCATTTGCTGATGAGTGAAGGACCCGCTTCAGACGTTGAGAGACACCCCTGGA 1548
| | | | |
QY 60 ArgTyrrProAspThrLeuLeuGlySerThrGluLeuGluPhePhePheAaGluAaPThr 79
| | | | |
Db 1549 CGTTACCCAGACACTCTACTGGGAGCTTCTGAGAGGAGACTTTTCTACCAACCCAGAACT 1608
| | | | |
QY 80 LysGluTyrrPhePheAspArgAspProGluValPheArgCysValLeuAaAaPheTyrrArg 99
| | | | |
Db 1609 CAGCAGATATTTCTTGAACCGTGAACCCAGACATCTTCGCGCACATCTGAAATTTCTACCC 1668
| | | | |
QY 100 ThrGlyIleLeuIleIstTyrrProArgTyrrGluCylSerAlaIstTyrrAspAspGluLeuAla 119
| | | | |

```

```

Db 1669 ACTGGGAAGCTCCACTATCTCCGCAAGAGTGATCTCTGCTTACATGATGAGAACTGGCC 1728
| | | | |
QY 120 PheTyrrGlyIleLeuProGluIleIleGlyAspCysTyrrGluGluTyrrLysAspArg 139
| | | | |
Db 1729 TTCTTGGCTCCATCCCGGAATCATCGCGAGCATGCTGTTATGAGAGTCAAGAGATCGC 1788
| | | | |
QY 140 LysArgGluAaAaIleGluArgLeuMetAspAspAsnAspSerGluAaAaAaGlnIleSer 159
| | | | |
Db 1789 AGCGAGAGAAACCGCGAGCCCTGCAAGACGACCGGATVACCAACACCGCTGGGGAGAGC 1848
| | | | |
QY 160 ---MetProSerLeuSerPheArgGlnThrMetThrArgAlaPheGluAaAaProIstThr 178
| | | | |
Db 1849 GCTTGGCCCAACATGACTGACAGGACAGAGGCTCTGAGAGGCTTTCAGAAACCCCAACCC 1908
| | | | |
QY 179 SerThrLeuAlaLeuValPheTyrrTyrrValThrGlyPhePheIleAlaValSerAlaIle 198
| | | | |
Db 1909 AGCAGATGGCCCTGGTGTCTTACTATGTCACGGGGTTTTTCATGTCGCTGTCATC 1968
| | | | |
QY 199 ThrAaAaValAlaGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
| | | | |
Db 1969 GCGAATGTGTGAAACAGTGCCTGCGGATCAAGCCAGGTCACTTAAGAACTGCCC 2028
| | | | |
QY 218 CysGlyGluArgTyrrSerValAlaPhePheCysLeuAaPThrAlaCysValMetIlePhe 237
| | | | |
Db 2029 TGTGAGAGCGCGTATGCTGTGCTTCTTCTGCTTGAACAGGCTGCTCATGATCTTC 2088
| | | | |
QY 238 ThrValGluTyrrLeuLeuArgLeuPheAlaAlaProSerArgTyrrArgPheIleArgSer 257
| | | | |
Db 2089 ACAGTTGAGTATTTGCTTCCGCTGCGCTGACAGCGCTAGTGGTTACCTGTTGGCGGAGT 2148
| | | | |
QY 258 ValMetSerIleIleAaAaValAlaIleMetProTyrrTyrrIleGlyLeuValMetThr 277
| | | | |
Db 2149 GTCATGATATCATCGACGTGTGCGCATCTGCTTATTAATGATGGCTGTGATACCA 2208
| | | | |
QY 278 AaAaAaGluAaPValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
| | | | |
Db 2209 GACATGAGACGTCACGAGAGCTTGTCTCACTCCGAGTCTCCGGCTTCAGAGATC 2268
| | | | |
QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrrThrLeuLysSerCys 317
| | | | |
Db 2269 TTTAAGTTTCCCGCACTCAAGCGCTGCGCATCTCGGGGTACACATGAAGAGTTGT 2328
| | | | |
QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
| | | | |
Db 2329 GCCTCAGAAATGGGCTTCTTGTCTTCTGCTCACCATGCTCACTCCGAGTCTCCGGCTTCAGAGATC 2388
| | | | |
QY 338 ValMetPheTyrrAlaGluLeuGlySerSerAlaSerIlePheThrSerIleProAlaSer 357
| | | | |
Db 2389 GTTATGTTCTACCGCAAGAAAGGGGCTTCGGCTAGCAAGTTCCACGACATCCCTGAGCC 2448
| | | | |
QY 358 PheTrpTyrrThrIleValThrMetThrThr-----ProLeuThrIleAlaGlyIlePhe 367
| | | | |
Db 2449 TTCTGTATATACCATCTGCTCACCATGACACCACTAGGCTAGTCCCATTAATGGAAATGGGA 2508
| | | | |
QY 368 -----LeuGlyTyrrGlyAspMetVal-----ProLeuThrIleAlaGlyIlePhe 383
| | | | |
Db 2509 TGGAGGTGGGTATGGGTAGCGCATTTGACCCCATCGAGTTACATGTAATCCGGG 2568
| | | | |
QY 384 GlySerIleCySerLeuSer 390
| | | | |
Db 2569 GAAATCATTTGTTTCTTCTCC 2589
| | | | |

```

## RESULT 17

```

US-10-029-386-24777/c
; Sequence 24777, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
; FILE REFERENCE: ABOMICA-X-2

```



CURRENT APPLICATION NUMBER: US/10/029,386  
 CURRENT FILING DATE: 2001-12-20  
 NUMBER OF SEQ ID NOS: 34288  
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
 SEQ ID NO 24777  
 LENGTH: 1121  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: MAP TO AF207550.1  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1  
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9  
 OTHER INFORMATION: SWISSPROT HIT: P17971, EVALU0.00e+00  
 OTHER INFORMATION: NT HIT: g14760095, EVALU0.00e+00  
 OTHER INFORMATION: EST\_HUMAN HIT: AL120075.1, EVALU0.00e+00  
 US-10-029-386-24777

## Alignment Scores:

Pred. No.:	1.24e-149	Length:	1121
Score:	1490.50	Matches:	279
Percent Similarity:	87.17%	Conservative:	47
Best Local Similarity:	74.60%	Mismatches:	7
Query Match:	43.68%	Indels:	3
	16	Gaps:	3

US-10-062-879-2 (1-655) x US-10-029-386-24777 (1-1121)

Qy 1 MetAlaiaGlyValAlaAlaATrPLeuProPheAlaATrAlaAlaAlaIleGlyTrpMet 20  
 Db 1121 ATGGCGGAGGCGCTGGCAGCTGGCTGCTTTGTCTGGGAGAGCAGCGAGCTGGCTG 1062  
 Qy 21 ProValAlaAaNCysPrometProLeuAlaProAlaAplySaMlySaMlySaMlySaMly 40  
 Db 1061 CCGCTGGCGCCAGCAACCTCTCCCGCCGACCGGCGGTGAAGGATCTCTGAGAGATGAG 1002  
 Qy 41 LeuIleValIleuAnValSerGlyAArgArpHeGlnTrpArgTrpThrThleuGlnArg 60  
 Db 1001 GTTCTGGGTGAAGCGTAGGAGGAGCGCTTGTGAGCTTGAAGATAATACCTGAGCGC 942  
 Qy 61 TyrProAspThrLeuLeuGlySerThrGluysGluPhePheAsnGluAspThrIys 80  
 Db 941 TACCCAGACACCTTGTCTGGCAGCTCGGAGAAATCTTCTACGATCGTACGACG 882  
 Qy 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100  
 Db 881 GAGTACTTCTTCGATCGGAGCCTGACATGTTCCGCCATGTGCTGAACCTTACCGAAG 822  
 Qy 101 GlyIysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
 Db 821 GGGCGGCTGCAATCCAGCGGAGAGTGCATCCAGGCTTCCAGCAAGAGCTGCTTTC 762  
 Qy 121 TyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrIleAspArgIys 140  
 Db 761 TACGGCTGCTTCCGAGCTAGTGTGCTGCTCTTGAAGAGTATCGGAGCCGAAG 702  
 Qy 141 ArgGluAsnAlaGluArgLeuMetCaspAspAsnAspSerGluAsnGlnGluSerMet 160  
 Db 701 AAGAGAGATGCGGAGCGCTGCGAGAGATGAGGAGAGAGCGGAGAGCGC--- 645  
 Qy 161 ProSerLeu-----SerPheArgIleThrMetCTPArgAlaPheGluAsnPro 176  
 Db 644 CCAAGCTGCGCAGCAGCAGCTCCCTGCGGAGCGGCTGCTGCGGCTTCCAGAGATCA 585  
 Qy 177 HisThrSerThrLeuAlaLeuValPheTyrTyrAlaThrGlyPhePheIleAlaValSer 196  
 Db 584 CACAGAGACACCGAGCGCTGCTTCTACTATGTGAACGGCTTCTTACGCGGTGTG 525  
 Qy 197 ValIleThrAsnValValGluThrValProCys-----GlyThrValProGlySerIys 214  
 Db 524 GTCATCGCAATGTGTGTGAGAGCATCCATCCATGCGCGCTGCAAGAGGTCTCAAG 465

Qy 215 GluLeuProCysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysVal 234  
 Db 464 GAGCAGCGCTGTGGCGAAGCTTCCACAGGCTTTTCTGATGACACAGCGCTGTGTA 405  
 Qy 235 MetIlePheThrValGluTyrIleuLeuArgLeuPheAlaIleProSerArgTyrArgPhe 254  
 Db 404 CTCATATTCAACAGGTGAATACCTCTCGGCTGTGTTCGCCGCCACCGCTTGCCTTC 345  
 Qy 255 IleArgSerValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeu 274  
 Db 344 CTGGAGAGTGTCAAGAGCTTATGAGCTGTGAGCTGTCCTTCTTCTTACCATGCGCTT 285  
 Qy 275 ValMetThrAsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgVal 294  
 Db 284 TTGTGGCCAAAGAACAGAGATGCTCTGGCGCTTGTTCACCTGCGGTGTCCGGGTG 225  
 Qy 295 PheArgIlePheIysPheSerArgHisSerGlnIleuArgIleuGlyTyrThrIleu 314  
 Db 224 TTTCGCACTTCAAGTCTCCAGGACTCACAGGCTTGAAGATCTGGGCTTACACACTC 165  
 Qy 315 LysSerCysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIle 334  
 Db 164 AAGAGCTGTGCTTGAAGCTGAGCTTCTCTCTTCTTCTTACCATGCGCATATCATC 105  
 Qy 335 PheAlaThrValMetPheTyrAlaGluIleGlySerSerAlaSerIysPheThrSerIle 354  
 Db 104 TTTCGCACTGTCACTTGTATGCTGAGAGGCGCAACAAAGACCACTTACAGCATC 45  
 Qy 355 ProAlaSerPheTyrTyrThrIleValThrMetThrIleu 368  
 Db 44 CCGCGGCTTCTGTATACCATGTGCACATGACCAAGCTT 3

## RESULT 18

US-10-212-677-256  
 ; Sequence 256, Application US/10212677  
 ; Publication No. US20030129192A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chenault, Ruth A.  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: McNeill, Patricia D.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C7  
 ; CURRENT APPLICATION NUMBER: US/10/212,677  
 ; CURRENT FILING DATE: 2002-08-02  
 ; NUMBER OF SEQ ID NOS: 288  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 256  
 ; LENGTH: 1597  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-212-677-256

## Alignment Scores:

Pred. No.:	1.92e-84	Length:	1597
Score:	887.00	Matches:	161
Percent Similarity:	90.00%	Conservative:	28
Best Local Similarity:	76.67%	Mismatches:	19
Query Match:	26.00%	Indels:	2
	15	Gaps:	2

US-10-062-879-2 (1-655) x US-10-212-677-256 (1-1597)

Qy 1 MetAlaiaGlyValAlaAlaATrPLeuProPheAlaATrAlaAlaAlaIleGlyTrpMet 20  
 Db 966 ATGGCGGAGGCGGTGAGAGCTGCTGCTTTCACAGGAGCGGCTATCGGCTGATG 1025  
 Qy 21 ProValAlaAaNCysPrometProLeuAlaProAlaAplySaMlySaMlySaMlySaMly 39  
 Db 1026 CCGTGTGCTTGGGCGCTATGCTGCTCCCGGAGGAGAGAGAAAGAACCCAGAT 1085

```

QY      40  GluLeu11eValLeuAenValSerGlyArgPheGlnThrTrpArgThrThrLeuGlu 59
      1086  GCTCTCATTTGCTGGAATGGAAGTGGACCCGCTTCAGACGTTGAGACACCCCTGGAA 1145
QY      60  ArgTyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThr 79
      1146  CGTTACCCAGACACTCTACTGAGGCACTTCTGAGAGGACTTTTCTACACCCAGAAACT 1205
QY      80  LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99
      1206  CAGCAGATATTTCTTTGACCGTGAACCGACATCTCCGACACATCTGGAATTTCTACCGC 1265
QY      100  ThrGlyLysLeuHisTyrTrpArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119
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QY      120  PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArg 139
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QY      140  LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSer 159
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QY      160  ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThr 178
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QY      199  ThrAsnValValGluThrValProCysGly 208
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US-10-361-811-256
; Sequence 256, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-256

Alignment Scores:
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Score: 887.00 Matches: 161
Percent Similarity: 90.00% Conservative: 28
Best Local Similarity: 76.67% Mismatches: 19
Query Match: 26.00% Indels: 2
DB: 17 Gaps: 2

US-10-062-879-2 (1-655) x US-10-361-811-256 (1-1597)
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QY      21  ProValAlaAsnCySPrometProLeuAlaProAlaAspLysAsnLysArg---GlnAsp 39
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; Sequence 256, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-256

Alignment Scores:
Pred. No.: 1,92e-84 Length: 1597
Score: 887.00 Matches: 161
Percent Similarity: 90.00% Conservative: 28
Best Local Similarity: 76.67% Mismatches: 19
Query Match: 26.00% Indels: 2
DB: 17 Gaps: 2

US-10-062-879-2 (1-655) x US-10-369-186-256 (1-1597)
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QY      21  ProValAlaAsnCySPrometProLeuAlaProAlaAspLysAsnLysArg---GlnAsp 39
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QY      160  ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHiserThr 178
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QY      179  SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
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GenCore version 5.1.6  
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Searched: 1202784 segs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Database: Issued Patents NA.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	3291.5	96.5	2104	3	US-09-142-791A-1
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6	2498.5	73.2	5333	4	US-09-949-016-957
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13	713.5	20.9	7056	4	US-09-949-016-14035	Sequence 14035, A
14	712.5	20.9	3004	4	US-09-949-016-324	Sequence 324, App
15	712	20.9	1994	4	US-08-527-152-1	Sequence 1, Appl1
16	704	20.6	1341	4	US-10-162-012-7	Sequence 7, Appl1
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18	697.5	20.4	4234	4	US-09-949-016-325	Sequence 325, App
19	696	20.4	1599	1	US-08-288-405A-9	Sequence 9, Appl1
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25	637	18.7	2494	4	US-09-181-339-6	Sequence 6, Appl1
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#### ALIGNMENTS

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Sequence 1, Application US/09178109  
Patent No. 6395477  
GENERAL INFORMATION:  
APPLICANT: Cockett, Mark I.  
APPLICANT: Dilks, Daniel W.  
APPLICANT: Chang, Ling, Hsai-Ping  
APPLICANT: Sokol, Patricia T.  
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
FILE REFERENCE: abd-98069  
CURRENT APPLICATION NUMBER: US/09/178,109  
CURRENT FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2121  
TYPE: DNA  
ORGANISM: human  
US-09-178-109-1

Alignment Scores:  
Pred. No.: 0  
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US-10-062-879-2 (1-655) x US-09-178-109-1 (1-2121)

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; GENERAL INFORMATION:  
; APPLICANT: Antoine Michel Bril  
; APPLICANT: Thierry Paul Gerard Calmejs  
; APPLICANT: Jean-Francois Simon Piere Faivre  
; APPLICANT: Jean-Luc Javre  
; APPLICANT: Sabine Rouanet  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30012  
; CURRENT APPLICATION NUMBER: US/09/142,791A  
; CURRENT FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: UK 9706377.0  
; PRIOR FILING DATE: 1997-03-27

PRIOR APPLICATION NUMBER: EP 97402971.2  
PRIOR FILING DATE: 1997-12-09  
PRIOR APPLICATION NUMBER: EP 97403007.4  
PRIOR FILING DATE: 1997-12-11  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 2072  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
US-09-142-791A-3

Alignment Scores:  
Pred. No.: 0 Length: 2072  
Score: 3403.00 Matches: 653  
Percent Similarity: 99.69% Conservative: 0  
Best Local Similarity: 99.69% Mismatches: 2  
Query Match: 99.74% Indels: 0  
Gaps: 0

US-10-062-879-2 (1-655) x US-09-142-791A-3 (1-2072)

QY 1 MetAlaAlaGlyValAlaAlaATPLeuProPheAlaArgAlaAlaAlaIleGlyTyrMet 20  
Db 1 ATGGCGGACGAGAGTTGCAGCTGGCTGCTTTGCCGGGCTGGCCATCGGGTGATG 60  
QY 21 ProValAlaAsnCySPrometProLeuAlaProAlaAspLysAlaValGlnAspGlu 40  
Db 61 CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCGCCGACAAAGCCGACAGATGAG 120  
QY 41 LeuIleValLeuAsnValSerGlyArgArpPheGlnThrTPArpThrLeuGluArg 60  
Db 121 CTGATGTCTTCAACGTAGTGGGAGAGGTTCCAGACTGGAGACCACTTGAGGCC 180  
QY 61 TyrProAspThrLeuLeuGlySerThrGluGluPhePheAsnGluAspThrLys 80  
Db 181 TACCCGACACCTGCTGGGACGACGAGAGAGATTCTTCAACGAGACACCAAG 240  
QY 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100  
Db 241 GAGACTTCTTTCGACCCGAGACCCCGAGGTGTTCGCTGGCTGCCAATTCTTACCGCAGC 300  
QY 101 GluLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
Db 301 GGGAGCTGACCTACCCGCTACAGATCTCTGCTACGACGAGACTGACCTTC 360  
QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArgLys 140  
Db 361 TAGGGATCTCTCCGGAGATCATGGGGACTGCTGCTACGAGAGTCAAGACCGCAG 420  
QY 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnLysMet 160  
Db 421 AGGAGAGAACCCGACGCGCTCATGACGACCAACTCGAGAACCAACAGAGATCCATG 480  
QY 161 ProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThrSerThr 180  
Db 481 CCGCTCGTCAAGCTTCCGACACCATGTGGGGCTTCGAGAACCCCAACACCAAGCAG 540  
QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
Db 541 CTGGCCCTGGCTTCTACTAGTGACTGGCTTCTTCACTGCTGTCTGGTCAATCAACAC 600  
QY 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220  
Db 601 GTGGTGAAGACGGGCGGTGGGACAGCTCCGGGACAGCAAGAGCTGCCCTGGGGAG 660  
QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
Db 661 CGCTACTCGGTGGCTTCTTCTGCTGACACGGCGTGCATGATCTTACCGTGAG 720  
QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
Db 721 TACTCTCGGGGCTTCTCGGGCTCCAGCGCTACCGCTTCACTCCGAGGTGATAGC 780

QY 261 IleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnGlu 280  
Db 781 ATCATGACGTGGTGGGCTCATATCCCTACTACATCGTGTGCATGACCAACAGAG 840  
QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
Db 841 GAGGTGCGGGCGCTTCTGTCAGCTCCGGGTCTTCGCGCTTCAAGATCTTCAAGTTT 900  
QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320  
Db 901 TCCCGCACCTCCAGGGCTGGCGATCTGGGTACACACTGAGAGACTGTGCTCCGAA 960  
QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
Db 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020  
QY 341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTyr 360  
Db 1021 TATCCGAGAAAGGCTCTCGGCGACAGTTCACAGATCCCTGCTGTTGGTAC 1080  
QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGly 380  
Db 1081 ACCATTGTCAACATGACACACTGGGATACGAGACATGTGTGCTAAGACATTGACGG 1140  
QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
Db 1141 AAGATCTTGCGCTCATCTCTCTTGAAGGCGTCTGTGATTTGCCCTGCCAGTCCCT 1200  
QY 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
Db 1201 GTGATTTGTTCCAATTACTTACCGGATTTACACAGAAATCAGAGCTGATTAACGAGG 1260  
QY 421 AlaGlnLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
Db 1261 GCACAAAGAGGCGCCCTTGGCAGGATCCGTGGCCAAACAGGACATTCGAATGCA 1320  
QY 441 TyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThrGlyThrPro 460  
Db 1321 TACCTGCACAGAACCCCAAGGGCTCTCAAGAGGCGTGAAGCTGACGGGACCCCA 1380  
QY 461 GluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHisIleLeuLeu 480  
Db 1381 GAAGAGAGACATGGGCAAGACCACTCACTATGAGAGCCAGCATCACTGCTG 1440  
QY 481 HisCysLeuGluLysThrThrGlyLeuSerTyrLeuValAspAspProLeuLeuSerVal 500  
Db 1441 CACTGCTGGAAAAAACCACTGGGTGTCTATCTTGTGATGATCCCTGTTATCTGTA 1500  
QY 501 ArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGluGlnAsnCys 520  
Db 1501 GAAACCTCCACCATCAAGAAACCAAGATTATGATAGAGAGATTGAGCAAGACTGC 1560  
QY 521 MetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSerSerHisPro 540  
Db 1561 ATGAGAGTTCAATGCAAGACTACCATCAACAAAGATCCCTCATCTGTCAGCAACCA 1620  
QY 541 GlyLeuThrThrThrCysCysSerArgArgSerLysThrThrHisIleLeuProAsnSer 560  
Db 1621 GGCTCACTACCACTGCTGCTCCCGCTGATGAAGAACCAACACCTGCCCAATTCCT 1680  
QY 561 AsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHisIleGlnGly 580  
Db 1681 AACCTGCACACTACTGCTGGCGAGATCAAGAGTCAAGACGATCCACATCCACAGG 1740  
QY 581 SerGluGlnProSerLeuThrThrThrSerArgSerSerLeuAsnLeuLysAlaAspAspGly 600  
Db 1741 AGTGAAGAGCCCTCCCTCAACACAGTCCCTCAGCTTAATTGAAGACAGACGAGA 1800  
QY 601 LeuArgProAsnCyLysThrSerGlnIleThrThrAlaIleIleSerIleProThrPro 620  
Db 1801 CTGAGACAAATGCAAAACATCCAGATCAACAGCCATCATCAGCATCCCACTGCC 1860



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QY      621 ProAlaLeuThrProGluGlyGlySerArgProProProAlaSerProGluProAlaThr 640
DB      1861 CCGGCGCTAACCCAGAGGGGAGAAAGTCGAGCCACCCCTGGCCAGCCCAAGCCCAACG 1920
QY      641 AsnIleProSerIleThrSerAsnValIleValSerValLeu 655
DB      1921 AACATTCCTTCCATACCGCAATGTTGTCAGAGTCTCCGCTTG 1965

RESULT 3
US-09-178-109-3
; Sequence 3, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Hwai-ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polypeptides and
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
US-09-178-109-3

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Alignment Scores:
Pred. No.:      0      Length:      2064
Score:          3300.50  Matches:      636
Percent Similarity: 97.10%  Conservative: 0
Best Local Similarity: 97.10%  Mismatches: 0
Query Match:      96.73%  Indels:      19
DB:               3      Gaps:      1

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US-10-062-879-2 (1-655) x US-09-178-109-3 (1-2064)

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QY      21 ProValAlaAsnGlySerProMetProLeuAlaProAlaAspIleAsnIleValArgGluAspGlu 40
DB      133 CCGGTGGCCAACTGCCCAATGCCCTGGCCCGCGGCGAACAAGACGAGGATGAG 192
QY      41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrTProArgThrThrLeuGluArg 60
DB      193 CTGATTGTCTCAACGAGTGGCGAGGTTCCAGACCTGGAGGACCAAGCTGAGAGCGC 252
QY      61 TyrProAspThrLeuLeuGlySerThrGluIleGlyPhePheAsnGluAspThrIle 80
DB      253 TACCCGGAACCTTGTCTGGGACACGAGAGAGAGTTCTTCTTCAACAGAGACCAAG 312
QY      81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100
DB      313 GAGTACTTCTTTCACCGGAGCCCGAGGTGTTCCGCGGTGCTCAACTTTCACGCAAG 372
QY      101 GlyIleLeuHisTyrProAlaGlyTyrGlyCysIleSerAlaTyrAspAspGluLeuAlaPhe 120
DB      373 GGGAGAGTGCACACCGCGCTACAGTGCATCTGCGCTACGACGACGAGGCTGCGCTTC 432
QY      121 TyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGlyGluTyrIleAspArgIle 140
DB      433 TACGGCACTCTCCCGGAGATCATCGGAGCTGCTACGAGGAGTACAGAGACCCAG 492
QY      141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGluGluSerMet 160
DB      493 AGGAGAGACCGCGAGCGGCTCATGAGACGACAGCACTCGGAGAGAACAGAGGTCCAG 552
QY      161 ProSerLeuSerPheArgIleThrMetTProArgAlaPheGluAsnProHisThrSerThr 180

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DB      553 CCTTCGCTACGCTTCCGCGAGCATGTGGCGGGCTTCCAGAAACCCCAACACAGCAG 612
QY      181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200
DB      613 CTGGCCCTGGGCTTCTACTAGTACTGAGTGGCTTCTTCATCGCTGTCTGCTCATCACCAAC 672
QY      201 ValValGluThrValProGlyGlyThrValProGlySerIleGluLeuProGlyGlyGlu 220
DB      673 GTGGAGAGAGAGGCGCGTGGCGAGCGTCCCGGAGCAAGAGAGCTGCGTGGGGAG 732
QY      221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240
DB      733 CGTACTCGGCGCTTCTTCTGCTGGAGACAGCGCGCTCATGATCTTACCGTGGAG 792
QY      241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260
DB      793 TACCTCGGCGGCTTCTCGGGCTCCAGCGCTACCGCTTCAATCCGACGTCATAGC 852
QY      261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280
DB      853 ATCATCAGACGTGGGCGCATATGCTTACTATCGTGTGTCATGATGACCAACAGAG 912
QY      281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheIlePhe 300
DB      913 GACGTGTCGGCGGCTTCTGTCAGCGCTCGGGTCTTCGGCTTTCAGATCTTCAAGTT 972
QY      301 SerArgHisSerGluGlyLeuArgIleLeuGlyTyrThrLeuIleSerCysAlaSerGlu 320
DB      973 TCCGCGCACTCCAGGCGCTGGGATCTGGGCTACACACTGAAGAGCTGTGCTCGAA 1032
QY      321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340
DB      1033 CTGGCTTCTTCTTCTTCTTCTTCCATCATGAGCATTCATCTTGGCACGTGATGTT 1092
QY      341 TyrAlaGluIleGlySerSerAlaSerIlePheThrSerIleProAlaSerPheTyr 360
DB      1093 TATGCCAGAGAGGCTCTCGGCGAGAGTTCAAGCATCCTGCTGCTTTGGTAC 1152
QY      361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIleThrIleAlaGly 380
DB      1153 ACCATTGTCACTAGACACACTGGATACGAGACATGAGTGTCTAAGATGACAGG 1212
QY      381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400
DB      1213 AAGATCTTCGCTCATCTGCTCTTGAAGTGGCGTCTGTCATGCTCCGCAATGCT 1272
QY      401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspIleArgArg 420
DB      1273 GTGATTGTTTCAACTTTAGCCGATTTTACCAACAGATCAGAGCTGATTAACGAG 1332
QY      421 AlaGluIleValAlaArgLeuAlaArgIleArgValAlaIleThrGlySerSerAsnAla 440
DB      1333 GCACAAAGAGAGGCGCGCTTGGCAGAGTCCGTGGCCAAACAGGACAGTTCGAATGCA 1392
QY      441 TyrLeuHisSerIleValAsnGlyLeuLeuAsnGluAlaLeuGluLeuThrGlyThrPro 460
DB      1393 TACCTGCACACAGACCGGACCGCTCTCAACAGCGCGTGGAGCTGAGGGGACCCCA 1452
QY      461 GluGluGluHisMetGlyIleThrThrSerLeuIleGluSerGlnHisHisIleLeuLeu 480
DB      1453 GAAAGAGGACACATGGGAGACCACTCATTCATGAGACGACGATCATCACTCTG 1512
QY      481 HisCysLeuGluIleThrThrGlyLeuSerTyrLeuValAspAspProLeuLeuSerVal 500
DB      1513 CACTGCCCGGAAAAAACACT----- 1533
QY      501 ArgThrSerThrIleIleValAsnHisGluPheIleAspGluGlnMetPheGluGlnAsnCys 520
DB      1534 -----AACACGAGATTATTATATAGCAGAGATTGGACGAACTGC 1575
QY      521 MetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerIleSerSerHisPro 540

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QY 401 ValIleValSerAsnDhSerArgIleYrHsGlnAsnGlnArgAlaAspLysArg 420  
Db 1201 GTGATTGTTCCAACTTACCGCGATTATCCACGAAATCAAGAGCGTATTAAGCGAG 1260  
QY 421 AlaGlnLysValAlaArgLysAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
Db 1261 GCAACAAAGAGGCGCGCTTCCAGAGATCCGTTGCGCAAAACAGGCGATTGCAATGCA 1320  
QY 441 TyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLysThrGlyThrPro 460  
Db 1321 TACCTGCACAGCAAGGCAACGGGCTCTTCAACAGAGCGCTGGAGTGAACGGCACCCCA 1380  
QY 461 GluGlnGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisIshisLeuLeu 480  
Db 1381 GAAGAGAGACACATGGGCAAGACCACTCATCATGAGAGCGCATCATCACTGCTG 1440  
QY 481 HisCysLeuGluLysThrThrGlyLysSerTyrLeuValAspAspProLeuLeuSerVal 500  
Db 1441 CACTGCTGCAAAAAACCACT----- 1461  
QY 501 ArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGluGlnAsnCys 520  
Db 1462 -----AACCAAGAGTTATTGATGAGACAGATGTTGAGCAGAACTGC 1503  
QY 521 MetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSerSerHisPro 540  
Db 1504 ATGAGAGATTCAATGACGAATCACTCCATCCACAAAGAGTCCCTCACTGTCAGCCACCA 1563  
QY 541 GlyLeuThrThrThrCysCysSerArgArgSerLysValThrThrHisLeuProAsnSer 560  
Db 1564 GGGCTCACTACACCTGCTGCTCCGCTGATGTAAGAGACACACACCTGCCCCAATCTT 1623  
QY 561 AsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHisIleGlnGly 580  
Db 1624 AACCTGCACACTCTGCGCTCGGACAGATGCAAGAGTCAAGATCCCAATCCAGGCG 1683  
QY 581 SerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAspAspGly 600  
Db 1684 AGTGAAGAGCCCTCCCTCCACACCAAGTCCGCTCCAGGCTTAATTGAAAGACAGCGGA 1743  
QY 601 LeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleSerIleProThrPro 620  
Db 1744 CTGAGACAAACGCAAAACATCCAGATACACACAGCATCATCACTCCCACTCCC 1803  
QY 621 ProAlaLeuThrProGluGluGluSerArgProProProAlaSerProGlyProAsnThr 640  
Db 1804 CCAGCGCTAACCCAGAGGGGGAAGTCCGCGCACCCCTGCGCAGCCCAAGCCCAACAG 1863  
QY 641 AsnIleProSerIleThrSerAsnValValLysValSerValLeu 655  
Db 1864 AACATTCCTTCATAGCCAGCAATGTTCAAGGTCTCCGCTTG 1908

RESULT 5  
US-09-142-791A-5  
; Sequence 5, Application US/09142791A  
; Patent No. 6368823  
; GENERAL INFORMATION:  
; APPLICANT: Antoine Michel Alain Brill  
; APPLICANT: Thierry Paul Gerard Calmeis  
; APPLICANT: Jean-Francois Simon Pierre Faivre  
; APPLICANT: Jean-Luc Javre  
; APPLICANT: Sabine Rouanet  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30012  
; CURRENT APPLICATION NUMBER: US/09/142, 791A  
; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: UK 9706377.0  
; PRIOR FILING DATE: 1997-03-27  
; PRIOR APPLICATION NUMBER: EP 97402971.2  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: EP 97403007.4

; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 2104  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-142-791A-5

Alignment Scores:  
Pred. No.: 0 Length: 2104  
Score: 3265.50 Matches: 630  
Percent Similarity: 96.34% Conservative: 1  
Best Local Similarity: 96.18% Mismatches: 5  
Query Match: 95.71% Indels: 19  
DB: 3 Gaps: 1

US-10-062-879-2 (1-655) x US-09-142-791A-5 (1-2104)

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QY 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArgGlnAspGlu 40  
Db 61 CCGGAGGCAACTCCCAATGCTCTGACCCCGGCGCAAGAACAGACGGCAGATGAG 120  
QY 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrThrArgThrThrLeuGluArg 60  
Db 121 CTGATTGTCCTCAACGATGAGGCGGAGGTTCCACAGCTGAGAGACACGCTGAGCGC 180  
QY 61 TyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThrLys 80  
Db 181 TACCGGACACCTCGCTGGGACGACGAGAGAGATTTCTTCAACGAGACCAAG 240  
QY 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100  
Db 241 GAGTACTTCTTCAACCGGAGCCCGAGGTGTTCCGCTGCTGCTCACTTACCGCAG 300  
QY 101 GlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
Db 301 GGGAACTGCACCTACAGCGCTACGAGATCTCTGCTACACAGACGAGCTGCTTC 360  
QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArgLys 140  
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QY 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnLysMet 160  
Db 421 AGGGAAGAGCGCGAGGCTCATGAGACACAGACCTCGAGAACACAGAGTCCATG 480  
QY 161 ProSerLeuSerPheArgGlnThrMetThrArgAlaPheGluAsnProHisThrSerThr 180  
Db 481 CCTGCTCAGCTTCGCGACACATGAGGCGGCTTCGAGAACCCCAACACAGCAGCAG 540  
QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaLysSerValIleThrAsn 200  
Db 541 CTGGCCCTGCTCTTACTACGTACGTGCTTCTTCACTGCTGCTGCTGCTATCAAC 600  
QY 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220  
Db 601 GTGGTGAAGAGGTCCTGCGGAGCGGCTCCCGGAGCAAGAGCTGCTGCGGGAG 660  
QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
Db 661 CGCTACTGCTGCTGCTTCTTCTGCTGAGACAGGCGTGCATGATCTTACCGTGGAG 720  
QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
Db 721 TACTCTCTGCGGCTCTTGGCGGCTCCAGCGCTACCTTCATCCGAGGTATGAGC 780  
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Db 781 ATCATGACGTGTGGCCATCATGCCCTAATCATCGGTCTGTCATGACCAACAGCAG 840  
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Db 841 GACGATCCGCGGCTTGTACGCTCCGGATCTTCGCGCTTCAGGATCTCCAGTTT 900  
Qy 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyThrLeuLysSerCysAlaSerGln 320  
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Db 1081 ACCATTGTACACATGACACACTGGGATACGGACATGTGCTTAAGACATTTGCAGGG 1140  
Qy 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
Db 1141 AAGATCTTCGGCTCATCTGCTCTTGAATGCGCTGCTGATTCATTCCTCCAGTCCCT 1200  
Qy 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
Db 1201 GTGATTTTTCACACTTATGCGGATTTTACACAGAAACAGACGATTAACGCAAG 1260  
Qy 421 AlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
Db 1261 GCACAAAGAGAGCCCGCTTGCAGACATCCGTGGCCAAAGAGCATTTCCAAATCA 1320  
Qy 441 TyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGlyLeuThrGlyThrPro 460  
Db 1321 TACCTGACAGCAGCAGCAGGAGGCTCTCAACAGAGGCGTGAAGCTGACGCGCACCCCA 1380  
Qy 461 GlnGlnGlnHisMetGlyLysThrThrSerLeuIleGlnSerGlnHisHisIleLeu 480  
Db 1381 GAAGAGAGACACAGGCGACAGACACCTCACTCAAGAGCAGCAGCATCACCCTGTG 1440  
Qy 481 HisCysLeuGlyLysThrThrGlyLeuSerTyrLeuValAspAspProLeuLeuSerVal 500  
Db 1441 CACTGCTGAAAACCACT----- 1461  
Qy 501 ArgThrSerThrIleLysAsnHisGlnPheIleAspGlnGlnMetPheGlnAsnCys 520  
Db 1462 -----AACCAAGATTATTTATGAGAGATGTTTGAACAGACTGC 1503  
Qy 521 MetGlnSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSerSerHisPro 540  
Db 1504 ATGAGAGGTTCAATGACAACTACCATCCACAGAAAGTCCCTCACTGCCAGCACCCA 1563  
Qy 541 GlnLeuThrThrThrCysCysSerArgArgSerLysLysThrThrHisIleuProAsnSer 560  
Db 1564 GGCTCACTACACACTGCTGCTCCGCTGTAAGTAAGAACCAACCACTGCCCAATTTCT 1623  
Qy 561 AsnLeuProAlaThrArgLeuArgSerMetGlnLeuSerThrIleHisIleGlnGly 580  
Db 1624 AACCTGCAAGTATTCGCGCTGCGAGCATGACAGACGATTCACATCAACAGGCG 1683  
Qy 581 SerGlnGlnProSerLeuThrThrThrArgSerSerLeuAsnLeuValAspAspGly 600  
Db 1684 AGTAGAGAGCCCTCTCCACAAACAGTGCCTCAAGCTTAATTGAAGAGAGAGAGCGGA 1743  
Qy 601 LeuArgProAsnGlyLysThrSerGlnIleThrThrAlaIleIleSerIleProThrPro 620  
Db 1744 CTGAGACCAAACTCCAAACATCCCAATTCACACAGCATCATCAGATCCCACTCC 1803  
Qy 621 ProAlaLeuThrProGlnGlyGlnSerArgProProAlaSerProGlyProAsnThr 640  
Db 1804 CCAAGCGTAACCCAGAGGGGGAAGTCCGACACCCCTGCGACGCCCGCCCAACACG 1863

Qy 641 AsnIleProSerIleThrSerAsnValValLysValSerValLeu 655  
Db 1864 AACATCTCTTCATACAGCCAGCAAGTGTGTCAAGGTCTCCGCTTG 1908

RESULT 6  
US-09-949-016-957  
Sequence 957, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CD001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 957  
LENGTH: 5333  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-957

Alignment Scores:  
Pred. No.: 1,676-241 Length: 5333  
Score: 2498.50 Matches: 486  
Percent Similarity: 84.09% Conserved: 69  
Best Local Similarity: 73.64% Mismatches: 70  
Query Match: 73.23% Indels: 35  
Gaps: 7

US-10-062-879-2 (1-655) x US-09-949-016-957 (1-5333)

Qy 1 MetAlaAlaGlyValAlaAlaATPLeuProPheAlaArgAlaAlaIleGlyTyrMet 20  
Db 966 ATGGCGGCGGGGGGAGCGAGTGGCTCTTTGCAAGGCGAGCGCTATCGGCTGATG 1025  
Qy 21 ProValAlaAsnGlyProMetProLeuAlaProAlaAspLysAsnLysArg---GlnAsp 39  
Db 1026 CTTGTGGCTTGTGTAATGTGATGGGCACTCCCGGAGGAGGAGAAAGCAACCAAGAT 1085  
Qy 40 GlnLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTyrArgThrThrLeuGln 59  
Db 1086 GCTTCAATTTGCTGAATGTGATGGGCACTCCCGGAGGAGGAGAAAGCAACCAAGAT 1145  
Qy 60 ArgTyrProAspThrLeuLeuGlySerThrGlnLysGlnPhePheAsnGlnAspThr 79  
Db 1146 CGTTACCAAGACACTTACAGGCGAGTTCGAGAGGACTTTTCTACACCCAGAAACT 1205  
Qy 80 LysGlnTyrPhePheAspArgAspProGlnValPheArgCysValLeuAsnPheTyrArg 99  
Db 1206 CAGCAGATATTTCTTGAACCGTGAACCCGACATCTTCGCGCAACCTCGAAATTTCTACCG 1265  
Qy 100 ThrGlnLysLeuHisTyrProArgTyrGlnCysIleSerAlaTyrAspAspGlnLeuAla 119  
Db 1266 ACTGGAGAGCTCACTATCTCTCGGCAAGTGCATCTCTGTTACGATGAAGACTGCG 1325  
Qy 120 PheTyrGlyIleLeuProGlnIleIleGlyAspCysArgTyrGlnGlnTyrLysAspArg 139  
Db 1326 TTTCTTGGCTCATCCGGAATCATGCGGCACTGCTGTTATGAGAGTACAAAGATCGC 1385  
Qy 140 LysArgGlnAsnAlaGlnLysGlnMetAspAspAsnAspSerGlnAsnGlnGlnSer 159  
Db 1386 AGGGAAGAGAACCGCGAGCGCTGCGAGACGACCGGATTCGACACCGCTGGGGAAGC 1445  
Qy 160 ---MetProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGlnAsnProHisThr 178

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Db      1446 GCCTTGCACCATGACGTGACAGGAGGCTGAGAGGCTTGCAGAACCCCAACAC
Qy      179 SerThrLeuAlaLeuValPheTyTyValThrGlyPhePheLeuAlaValSerValIle
Db      1506 AGCAGATAGGCTCGGTGTTCTACTATGTCACGGGGTTTTTTCATGCGCTCTGTCATC
Qy      199 ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro
Db      1566 GCCAAATGTGTGAAACAGTGCCTGCGGATCAAGCCAGGTCACTTAAGAAACTGCCCC
Qy      218 CysGlyGluArgTySerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe
Db      1626 TGTGAGAGAGCGGATATGCTGTGCTCTTCTGTTGAGACAGCGCTGCTGATGATCTTC
Qy      238 ThrValGluTyLeuLeuArgLeuPheAlaAlaProSerArgTyArgPheIleArgSer
Db      1686 ACAGTTGAGATATTTGCTTCGCTGCGTGCAGCGCTAGTCGTATCCGTTTGGCTAGT
Qy      258 ValMetSerIleIleAspValAlaAlaMetProTyTyTrIleGlyLeuValMetThr
Db      1746 GTCATAGATATCATCAACGTGTGCGCATCTGCTTATTAATGAGGCTGTGATGACA
Qy      278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle
Db      1806 GACAAATGAGAGACTGACGGAGCTTGTTCACACCTCGAGTCTTCGGGGTCTTCAGGATC
Qy      298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyTrThrLeuLysSerCys
Db      1866 TTTAAGATTTTCCCGCACCTCTCAAGGCTGCGCATCTGGGGGTACACATGAAGAGTTGT
Qy      318 AlASerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr
Db      1926 GCCTCAGAAATGTGGCTTCTTGTCTTCTGCTCACATGCTATCATCATCTTCGCTACA
Qy      338 ValMetPheTyAlaGluLysGlySerSerAlaSerIlePheThrSerIleProAlaSer
Db      1986 GTTATGTCTTACCGCAGAAAGGGGCTTCGGCTAGCAAGTTCACCGCATCCTGTGAGCC
Qy      358 PheTrpTyThrIleValThrMetThrThrLeuGlyTyTrGlyAspMetValProLysThr
Db      2046 TTTCTGGATACCATGTCACCATGACAAACATAGGGATGATGATGATGATGATGATGATG
Qy      378 IleAlaGlyValIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu
Db      2106 ATAGCAGGAGAAATTTTGTGTTCTATCTGTTCTGCTGATGAGGGGCTTGTGCTGCTCA
Qy      398 ProValProValIleValSerAsnAspSerArgIleTyTrHisGlnAsnGlnArgAlaAsp
Db      2166 CTTGTTCCGATGATGATCAACTTCATGTCGATCTTACCAACAGATCAACAGACGACG
Qy      418 LysArgAlaArgAlaGluLysValAlaArgLeuAlaArgIleArgValAlaLysThrGlySer
Db      2226 AAACGAAAGGCAAAAGAAAGTAAGCTGCGCAGGATCCGGGACAGCAAAAGCGGAGAC
Qy      438 SerAsnAlaTyLeuHisSerIleArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr
Db      2286 GCAAAATGCTTACATGACGACAAACGGAATGTTTACTCATCATGATCAGCTGACG---TCC
Qy      458 GlyThrProGluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis
Db      2343 TCAGAGATAGACAGGCTTTTGTGTAAGCAAAATCCGGCTTCACGCTTTAAACCCAGCACG
Qy      478 HisLeuLeuHisCysLeuGluLysThrThrGlyLeuSerTyLeuValAspAspProLeu
Db      2403 CACCTGCTTACATGCTCGAAGAAAACACAGC-----
Qy      498 LeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGlu
Db      2433 -----AATCAGAGATTTGTGAGCAACAAAGCTTTTGAA
Qy      518 GlnAsnCysMetGluSerSerMetGlnAsnTyProSerThrArgSerProSerLeuSer

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Db      2466 GAAGCTGATGAAAGTTGCAACTGTATGTCCTTCAAGTCAACAGTCTTCACTGCT
Qy      538 SerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysLysThrHisLeu
Db      2526 TCACAAACAGAGAGCACACACACCTGCTGTTCAGAGACAAACAACTTTTCCGATC
Qy      558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHis
Db      2586 CCMAATGCAATGTATACAGAAAGCATCAAGATGATGATACAAAGTCCACAGATTCAG
Qy      578 IleGlnGlySerGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLysAla
Db      2646 ATCAGATGTGTGAGAGAAACCTCTGTCTAACAGCGCATTCAGATTAAATGCCAAATG
Qy      598 AspArgGlyLeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleIleSerIle
Db      2706 GAAGAGTGTGTAACTTAACTGAAACCACTTATGTGACTACAGCAATTAATGATC
Qy      618 ProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAlaSer
Db      2786 CCMACTCTCCAGTACACCAACCGAAGAGAGATGATGCGCAGATCCCTGAGTACTCA
Qy      636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerValLeu
Db      2826 GAAGGA-----AATATGTGAGAGTTCTGCTTTG
RESULT 7
US-09-336-643A-9
; Sequence 9, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutler, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3424
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1257)...(2195)
; OTHER INFORMATION: K-Hnov12
US-09-336-643A-9
Alignment Scores:
Pred. No.: 6,29e-202 Length: 3424
Score: 2104.00 Matches: 429
Percent Similarity: 74.78% Conservative: 78
Best Local Similarity: 63.27% Mismatches: 117
Query Match: 61.66% Indels: 54
DB: Gaps: 14
US-10-062-879-2 (1-655) x US-09-336-643A-9 (1-3424)
Qy      1 MetAlaAlaGlyValAlaAlaAlaTrpLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet
Db      257 ATGGCGGAGGCGCTGGCGACAGCTGCTGCTTTTCTGCGGCGAGCAGAGTGGCGCTGCTG
Qy      21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArgGlnAspGlu

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Db 317 CCCCAGCCAGCAACCCCTGCCCCCGGACCGGGGGTGAAGCATCTCGAGGAGATGAG 376
Qy 41 LeuileValleuamValSerGlyValArgPheGlnThrPargThrThrLeuGluArg 60
Db 377 GTTCGTGTGTGAACGTGAACCGGCGCTTTGACCTTGGAAGAAATACGCTGGAACGC 436
Qy 61 TyrProAspThrLeuLeuGlySerThrGluGlnGluPhePheGlnGluAspThrLys 80
Db 437 TACCCAGACACTTGTGCTGGGAGCTCGAAGAAATTTCTTCTACGATGCTGACTCAGGC 496
Qy 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100
Db 497 GAGACTCTTTCATGTCGACACCTGACATGTTCCGACATGTCGTAACCTTACCGAAG 556
Qy 101 GlyValLeuHisTyrProArgTyrGluCysGlnSerLysTyrAspArgGluLeuAlaPhe 120
Db 557 GGGCGGCTGATGGCCACGCGGAGAGTGCATCCAGGCTTCGACGAAGAGCTGGCTTTC 616
Qy 121 TyrGlyLeuLeuProGluLeuLeuGlyAspCysThrGluGluTyrLysAspArgLys 140
Db 617 TACGGCTGTGTCCGAGCTAGTCGATGACTGCTGCTTGAGAGTATCGGACCGAAG 676
Qy 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSerMet 160
Db 677 AAGGAGATCCGAGCGCCCTGCGACAGATGAGGAGGACAGACGCGGGAGACGC--- 733
Qy 161 ProSerLeu-----SerPheArgGlnThrMetTyrPargAlaPheGluAsnPro 176
Db 734 CCAGCCCTGCGACAGGACGACCTCCCTGCGGACGCGCTCTGCGGGGCTTCGAAATCCA 793
Qy 177 HisThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheLeuAlaValSer 196
Db 794 CACACGACGACCGGAGCCCTGTTTCTACTATGTGACGCGCTTTCATCGCCGTGCG 853
Qy 197 ValIleThrAsnValValGluThrValProCys-----GlyThrValProGlySerLys 214
Db 854 GTATCGCCCAATGTGTGTGAGACATCCATCGCGGCTCTGACCGCAGGCTCTCAAG 913
Qy 215 GluLeuProCysGlyArgTyrSerValAlaPhePheCysLeuAspThrAlaCysVal 234
Db 914 GACGAGCCCTGTGGCGAAGCCTTCCACAGGCTCTTTTCTGACGACAGCAGCTGTGTA 973
Qy 235 MetIlePheThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPhe 254
Db 974 CTGATATTACACAGTGAATCTCTGCGCTGTTTCCGCGCCACCGCTTGCCTTC 1033
Qy 255 IleArgSerValMetSerIleLeuAspValValAlaIleMetProTyrTyrIleGlyLeu 274
Db 1034 CTGCGAGTGTCAAGGCTCATGACCTCATGACGTGTGGCCATCTGCGCTTACTACATTGGGCTT 1093
Qy 275 ValMetThrAsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgVal 294
Db 1094 TTGGTGTCCCAAGAACGACGATGTCTGTGGCGCTTTGTTCACCTCGCGTGTCCGGGTG 1153
Qy 295 PheArgTyrIlePheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeu 314
Db 1154 TTTCGACATCTTCAAGTCTCAGGCACTCAAGGCGCTTGAGGATTCGGGCTTACACATC 1213
Qy 315 LysSerCysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIle 334
Db 1214 AAGAGCTGTGCTGTGAGCTGGGCTTCTCTCTTTTCCCTTACCAATGCGCATATCATC 1273
Qy 335 PheAlaThrValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIle 354
Db 1274 TTGGCCACTGTCAATGTTTATGCTGAAGAAGGCAACAAACCACTTACAGATC 1333
Qy 355 ProAlaSerPheTyrPyrThrIleValThrMetThrThrLeuGlyTyrArgLysAspMetVal 374
Db 1334 CTGCGGCTTCTGTGATACCATGTCAACATGACCGCTGGCTACGAGACATGCTG 1393
Qy 375 ProLysThrIleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuVal 394

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Db 1394 CCGACACCATTCGTGGCAAGATTTTCGGGTCCATCTGCTCACTGAGTGGCTTGTGTC 1453
Qy 395 IleAlaLeuProValProValIleValSerAsnPheSerArgTyrIleGlnAsnGln 414
Db 1454 ATTGCCCTGCTGTGCCAGATGATGTGTCCAACTTTAGCCGATCTTCCACCGAACCAG 1513
Qy 415 ArgAlaAspLysArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLys 434
Db 1514 CGGGCTTACAAAGCGCGACGACAGCAGAGAGTGCGCTTGGCAAGATCCGATTGGCAAG 1573
Qy 435 ThrGlySerSerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeu 454
Db 1574 AGTGTATCCACCAATGCTTCTTCCAGTACACACAGAAATGAG-----GGCCTT 1621
Qy 455 GluLeuThrGlyThrProGluGluGlnHisMet-----GlyLysThrThrSerLeuIleGlu 473
Db 1622 GAGAGACGCGGAGTGGCGGAGAACAGGCTTTGTGTCCAGAAACGTTTGCCTTGGAA 1681
Qy 474 SerGlnHisHisLysLeuHisCysLysGluLysThrThrGlyLeuSerTyrLeuVal 493
Db 1682 CAGACATACACCACTTGGCTGCACTGTATAGAGAACAG----- 1723
Qy 494 AspAspProLeuLeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGlu 513
Db 1724 -----TGCATGATTCACAGATGAG 1744
Qy 514 GlnMetPheGlnGlnAsnGlyMetGluSerSerMetGlnAsnTyrProSerThrArgSer 533
Db 1745 CTCACCTTCAGTAA---GCCCTGGAGCGCTCTCGCGGGGTGGCGACACCGGAGC 1801
Qy 534 ProSerLeuSerSerHisPro-----GlyLeuThrThrThrCysCysSerArg 549
Db 1802 ACCTGTGTCTTCCAGCGAGTGGAGCCGGAAGCTGTGTCTTCTGCTGCTGCTGCTG 1861
Qy 550 ArgSerLys---LysThrThrHisLysProAsnSerAsnLeuProAlaThrArgLeuArg 568
Db 1862 AGGCGAAGCGCGCGCCATCCGCTTGCACATCCACTGCTCCTCAGCACGCTT---GGC 1918
Qy 569 SerMetGlnGluLeuSerThrIleHisIleGlnGlySerGluGlnProSerLeuThrThr 588
Db 1919 AGATGACGAGGTGAGCATG-----CTGACAGGCTGTGGCAGAGACCATGCCCTCAG 1972
Qy 589 SerArgSerSerLeuAsnLeuLysAlaAspAspGlyLeuArgProAsnCysLysThrSer 608
Db 1973 AGCGCTCCAGCTCATGACCAAGCCCGCATGACAGCTTACCTGAACTGACAGACGCG 2032
Qy 609 GlnIleThrThrAlaIleIleSerIleProThrProProAlaLeuThrProGluGlyGlu 628
Db 2033 GACTGTGTGCTGCATATACAGATCCCTAACCCCTCTGCAACACCCAGAT---GAG 2089
Qy 629 SerArgProProAlaSerProGly----- 637
Db 2090 AGCCAA-----CCTTCTCTCCCTGGGCGGTGGCGAGGCGCGGACACCTCAGGAAAC 2143
Qy 638 ProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerValLeu 655
Db 2144 TCAGCTGTGGTACCTTCTCTTCCCGGACACTGTCAAGATCTATCTCCTG 2197

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## RESULT 8

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US-09-949-016-2456
; Sequence 2456, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT FILING DATE: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

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QY 144 AlaGluArgLeuMet-----AspAspAsnAsp 152  
Db 480 GCGGAGAGGGGTGACATCTTGAGACCCCGACCTCATTTGGCGGAGACCCGCGAC 539  
QY 153 SerGluAsn-----AsnGlnGlnSerMetProSerLeuSer----- 164  
Db 540 GACGAGAGACCTGGCGCCAGAGCGCTGGGACATCGACGCGCGGGGCTCGGGGGCCCC 599  
QY 165 -----PheArgGlnThrMetThrPheGluAsn 175  
Db 600 GACGCGCAATCTGCCCTGAGAGAGCGCTGACCCCGCATGTGGCCCTTCTGAAAGAC 659  
QY 176 ProHisThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheLeuAlaVal 195  
Db 660 CCGTACTCGTCCAGAGCGCGCAGGTTTATGCTTTGGCTTCTTATCTTATCTGCTGTT 719  
QY 196 SerValIleThrAsnValIleGluThrValProCysGlyThrValProGlySerGly 215  
Db 720 TCATATTCAACTTTTTCCTGGAACACATGAGCTTTCATATTTGTTAAAAACAGACA 779  
QY 216 LeuProCysGlyGluArgTyrSerVal-----Ala 225  
Db 780 GAACCGCATCATCAATGCGACAAAGTGTGTTCTACAGTATGAATTTAAACGATCTGCC 839  
QY 226 PhePheCysLeuAspThrAlaCysValMetIlePheThrValGluTyrLeuLeuArgLeu 245  
Db 840 TTGACGATATGTAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 899  
QY 246 PheAlaIleProSerArgTyrArgPheIleArgSerValMetSerIleIleAspValVal 265  
Db 900 GTTTTTCACCCCAATAAATTGAATTCATCAAAATCTCTGAATATCATGACTTTGTG 959  
QY 266 AlaIleMetProTyrTyrIle-----GlyLeuValMetThrAsnGln 280  
Db 960 GCCATCTTACCTTCTTCTAAGAGTGGAGCTCAGTGGCGCTCATCCAAAGCTGCTAA 1019  
QY 281 AspValSerGlyAlaPheValIleThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
Db 1020 GATGTGCTTGCTTCTCAGAGGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1079  
QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320  
Db 1080 ACCGCGCATTTTGAAGTCTGAGGCTGCTGTGACATCACTTTCAGAGTACGATCAATGAA 1139  
QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThrValMetPhe 340  
Db 1140 TTTTGTGCTGTGATTAATTTCTGTGCTGTGAGAGTTTGTGATTAATTTGTACCATGATCTAC 1199  
QY 341 TyrAlaGluLys-----GlySerSerAlaSerLysPhe 351  
Db 1200 TATGCCAGAGAGAGTGGAGCTCAACCTAACGACCTTACGTTAGTACACACACAGTTTC 1259  
QY 352 ThrSerIleProAlaSerPheTyrTyrThrIleValThrMetThrThrLeuGlyTyrGly 371  
Db 1260 AAAAACAATTCCTCATTTGCTGTGGGCTGTAGTACGATGATCACTCCGTGGTTAAGGG 1319  
QY 372 AspMetValProLysThrIleAlaGlyLysIlePheGlySerIleCysSerLeuSerGly 391  
Db 1320 GATATGTACCCCGCAACATGTGTGAGCATGTGTGTGGAGCCCTGTGTGCTGTGGTGA 1379  
QY 392 ValLeuValIleAlaLeuProValProValIleValSerAsnPheSerArgIleTyrHis 411  
Db 1380 GTGTGTGCAATAGCAGTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1436  
QY 412 GlnAsnGlnArgAlaAspLysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArg 431  
Db 1437 TCTTGGCAATGCGAAAGCAAACTTCCAGAGAAAGAAAGAG-----CACATCCCT 1490  
QY 432 ValAlaLysThrGlySerSerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsn 451  
Db 1491 CTTGCTCTCAGGAGACTGACCTTACTTTTTCAGAGAGCAATTAATTAATGAGCTGCAAT 1550  
QY 452 GlnAlaLeuGlnLeuThrGlyThrProGlnGlnGlnIleHisMetGlyLysThrThrSerLeu 471

Db 1551 -----AGTACACAGAGTACACATGTCTGGCAAGCAATTCGACTT 1592  
QY 472 IleGlnSerGlnHisIleLeuLeuHisCysLeuGlnLysThrThrGlyLeuSerTyr 491  
Db 1593 CTGGAA-----CATTAACAGATCAGTGTATTCAGGTACACACATTAACAGAAAGTACCG 1646  
QY 492 LeuValAspAspPro-----LeuLeuSerValArgThrSerThrIleLysAsnHisGluPhe 510  
Db 1647 CCATATACACCCCGAGAAAGCTCCCATCAGACGCTCTAGTACAGACAAAGAGAGA 1706  
QY 511 IleAspGlnGlnMetPhe-----GlnGlnAsnCysMetGlnSerSerMet 525  
Db 1707 AGAGGGGAAACAGTTTCTTCTACTGACGACAGTGAATTAACGTTGTCTTGATGAGAG 1766  
QY 526 GlnAsnTyrProSerThrArgSerProSerLeuSerSerHisIleProGlyLeuThrThr 545  
Db 1767 ATCAGAAAGATATGAATAATCCGAAAGCTTAAACAACTAGCGGGCTTGGCAGGCAAT 1826  
QY 546 CysCysSerArgSerLysThrThrHisIleuProAsnSerAsnLeuProAlaThr 565  
Db 1827 -----GCTGAGGCTCTCTCCAGTAACTACACCTTCACTCTTGTCTGTAGG- 1880  
QY 566 ArgLeuArgSer 569  
Db 1881 CGCTCTCGATCT 1892

RESULT 10  
US-07-955-916-6  
Sequence 6, Application US/07955916  
Patent No. 5397702  
GENERAL INFORMATION:  
APPLICANT: CAHALAN, Michael D.  
APPLICANT: CHANDY, Kanithara G.  
APPLICANT: GRISMER, Stephen  
APPLICANT: GHANSHANI, Sanjin  
APPLICANT: GUTMAN, George A.  
APPLICANT: DETLEERS, Brent A.  
TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE  
TITLE OF INVENTION: DISEASES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Walter H. Dregler  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/955,916  
FILING DATE: 19921002  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregler, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-54474-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1805 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-07-955-916-6





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US-10-062-879-2 (1-655) x US-09-949-016-2293 (1-3004)
Qy 18 G1YTrpMetProValAlaAsnGys-----PrometPro 28
Db 142 GGGGCCCCGCTCAAGCGCGGTGGCGGCGCGCTGCGACCGCTACGAGCCCGCTCGCG 201
Qy 29 -----LeuAlaProAlaAspLysAsnLysArgGlnAspGluLeuIleValLeuAsnVal 46
Db 202 CCTCATCTCCGCGCGCGCGGAGAGAGACCTGCTCGCGGAGCGCGGTGATCATCAATC 261
Qy 47 SerG1YArgArgPheGlnThrTrpArgThrThrLeuGluArgTyrrProAspThrLeuLeu 66
Db 262 TCGGGGCTGCGCTCGAGACGAGCTGAGACCTTTGCGCGAGTTCCCGAGACGCTGCTG 321
Qy 67 G1YSerThrGluLysGluPhe---PhePheAsnGluAspThrLysGluTyrrPhePheAsp 85
Db 322 GGGGACCCCAAGCGCGCATGAGGTACTTCCGACCGCGTCCGCAACGAGTACTTCTCGAC 381
Qy 86 ArgAspProGluValPheArgCysValLeuAsnPheTyrrArgThr---G1YLeuLeuHis 104
Db 382 CGGACCGCGCGCGCTTCAAGCGCTTCTACTACTACTACTACTCGCGGCGCGCATCGCC 441
Qy 105 TyrProArgTyrrGluCysIleSerAlaTyrrAspAspGluLeuAlaPheTyrrG1YLeu 124
Db 442 CGGCGCGGTCAACGTCGATCGACATTTCTCGAGAGAGATCGCGTTCTACAG----- 495
Qy 125 ProGluIleIleG1YAspCysCysTyrrGluGluTyrrLysAspArgLysArgGluAsnAla 144
Db 496 -----CTGGCGCGAGAGCGCATGAGAGATTCCGCGAG----- 528
Qy 145 GluArgLeuMetLysAspAsnAspSerGluAsnAsnGlnLysSerMetProSerLeuSer 164
Db 529 -----GACGAGGCGCTTCTCTCGGAGAGAGAGCGCGCTTGGCCCCCGCGGAC 576
Qy 165 PheArgGlnThrMetTrpArgAlaPheGluAsnProHisThrSerThrLeuAlaLeuVal 184
Db 577 TTCAGGCGGACGAGGTGCTGCTTTCGAGTACCCGAGAGCTCGGAGCGCGCGCGGCGC 636
Qy 185 PheTyrrTyrrValThrGlyPhePheIleAlaValSerValIleThrAsnValGluThr 204
Db 637 ATCGCCATCGTTCGCGTGTGTCATCTCTCATCTTCATTGATCTTCTGCGTGGAGACG 696
Qy 205 ValProCysG1YThrValProG1YSerLysGluLeuProCys----- 218
Db 697 CTGCGC-----GAGTTCGCGACGAGAGAGACTACCCCGCTCGACGTGCGAGACTCA 750
Qy 219 -----G1YGluArg-----TyrSerVal 224
Db 751 TTGGAAGCAGCGCGGCAACAGACAGTGGGCGTCCGCGAGAGCTTCAGCTTCCGAT 810
Qy 225 AlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGluTyrrLeuLeuArg 244
Db 811 CCTTCTTGCGTGTGGAGAGCGTGTGCATCATCTGTTCTTCGAACTGCTGTGCGG 870
Qy 245 LeuPheAlaAlaProSerArgTyrrArgPheIleArgSerValMetSerIleIleAspVal 264
Db 871 TTCTTGGCTTGTCTTACAAAGCCACCTTCTCGGAAACATCAAGACCTGATGACATT 930
Qy 265 ValAlaIleMetProTyrrTyrrIleG1YLeuValMet-----Thr 277
Db 931 GTGGCCATCATCTCTTATTATCATCTGTGGTACCGAGCTGCGCGCAACAGAGGCAAT 990
Qy 278 AsnAsnGluAspValSerG1YAlaPheVal---ThrLeuArgValPheArgValPheArg 296
Db 991 GGAAGAGGCGCATGTCTCTGCGCATCTGAGGGTCAATCCGCGCTCAAGGGGTCTTCCG 1050
Qy 297 IlaPheLysPheSerArgHisSerGlnG1YLeuArgG1YLeuG1YTyrrThrLeuLysSer 316
Db 1051 ATCTTCAAGCTGTGCGCGCATCTCAAGGGGTGAGATCTCTCGGCGCAAGCGTGAAGCG 1110
Qy 317 CysAlaSerGluLeuG1YPheLeuLeuPheSerLeuThrMetAlaIleIlePheAla 336

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Db 1111 TCATGCGGAGCTGGAGTCTCATCTCTCTTTATTTGGGTCATCTTTTCTCC 1170
Qy 337 ThrValMetPheTyrrAlaGluLysG1YSerSerAlaSerLysPheThrSerIleProAla 356
Db 1171 AGCGCGTCTTACTTTCGCGAGGAGAGAGACCCCACTTCAAGTTTACAGACATCCGGAT 1230
Qy 357 SerPheTrpTyrrThrIleValThrMetThrThrLeuG1YTyrrG1YAspMetValProLys 376
Db 1231 GCCTTCTGTGGGAGGTGATACCATGACAACAGTGGTTACGGCGATATGACCCAGTG 1290
Qy 377 ThrIleAlaG1YLysIlePheGlySerIleCysSerLeuSerG1YAlaLeuValIleAla 396
Db 1291 ACCATAGGGGCAAGATTTGGGATCTCTGTGGCCATCCCGGTGTCTTGACCATGCA 1350
Qy 397 LeuProValProValIleValSerAsnPheSerArgLysTyrrHisGlnAsnGlnArgAla 416
Db 1351 TTGCGAATTCCTCCGATGTGTTTCCAACTTCAATTAATTCTTACCAACGGAGACAAAGCG 1410
Qy 417 AspLysArgArg-----AlaGlnLysAla 425
Db 1411 GAAGAGCAATCCAGTACATGACAGTGGGAAGTTGCCAGACCTCTCTTACGCGGAG 1470
Qy 426 ArgLeuAlaArgIleArgValAlaLysTyrrG1YSerSerAsnAlaTyrrLeuHisSerLys 445
Db 1471 GAGCTCCGAAAGCAAGAGATTAATCGACTGTGAGTAAGTCGAGATATAGTATCGAA 1530
Qy 446 ArgAsnG1YLeuLeuAsnGluAlaLeuGluLeuThr 457
Db 1531 GAGGCGGTATGAAACCATGACGCTTTCGCCAGAC 1566

RESULT 12
US-09-949-016-12066
; Sequence 12066: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12066
; LENGTH: 7055
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12066

Alignment Scores:
Pred. No.: 9,51e-61 Length: 7055
Score: 713.50 Matches: 167
Percent Similarity: 53.46% Conservative: 96
Best Local Similarity: 33.94% Mismatches: 160
Query Match: 20.91% Indels: 69
Gaps: 12

US-10-062-879-2 (1-655) x US-09-949-016-12066 (1-7055)
Qy 18 G1YTrpMetProValAlaAsnGys-----PrometPro 28
Db 2142 GGGGCCCCGCTCAAGCGCGGTGGCGGCGCGCTGCGACCGCTACGAGCCCGCTGCGCG 2201
Qy 29 -----LeuAlaProAlaAspLysAsnLysArgGlnAspGluLeuIleValLeuAsnVal 46
Db 2202 CCTCATCTCCGCGCGCGCGGAGAGAGACCTGCTCGCGGAGCGCGGTGATCATCAATC 2261

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Qy 105 TyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPheTyrGlyIleu 124
Db 2442 CGGCGGCGCAACGCGCCATGACATTTTCTCCGAGAGATCCGCTTACAG----- 2435
Qy 125 ProGluIleIleGlyAspCysCysTyrGluIuTyrIlyAspArgLysArgGluAsnAla 144
Db 2496 -----CTGGCGAGAGAGGCGATGAGAAATTCCGCGAG----- 2528
Qy 145 GluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSerMetProSerLeuSer 164
Db 2529 -----GACGAGGCGCTTCTCGCGGAGAGAGAGCGCGGCGCTTCCGCGCGAC 2576
Qy 165 PheArgGlnThrMetTyrArgAlaPheGluAsnProHisThrSerThrLeuAlaLeuVal 184
Db 2577 TTCCAGCGCCAGGAGTGTGCTGCTTTCGAGTACCCCGAGAGCTCCGGCGCGCGGCG 2636
Qy 185 PheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsnValIleGluThr 204
Db 2637 ATCGCCATCGTGTGCGTGTGCATCTTCATTCATTCATTCATTCGCTGAGACG 2696
Qy 205 ValProCysGlyThrValProGlySerIlyGluLeuProCys----- 218
Db 2697 CTGCGCG-----GAGTTCGCGAGAGAGAGACTACCCGCTCGACGTCGAGAGACTCA 2750
Qy 219 -----GlyGluArg-----TyrSerVal 224
Db 2751 TTCCAGACGCGCGCAACAGACGTCGCGGCGCGCGCGAGAGCGCTTCCAGCTTCCGAT 2810
Qy 225 AlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGluTyrLeuLeuArg 244
Db 2811 CCCTTCTTGCGTGTGAGAGACGCTGTGCATCATCTGTTCTCTTCCGAACTGCTGTGCG 2870
Qy 245 LeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSerIleIleAspVal 264
Db 2871 TTCTTCCTGCTGTCTACCAAGCAACCTTTCGCGAACAATCAATGACTGATGACATT 2930
Qy 265 ValAlaIleMetProTyrTyrIleGlyLeuValMet-----Thr 277
Db 2931 GTGGCCATCATCTCTTATTTATATCATCTGGGTACCGAGCTGCGCGCAACGAGCGCAT 2990
Qy 278 AsnAsnGluAspValSerGlyAlaPheVal---ThrLeuArgValPheArgValPheArg 296
Db 2991 GGAAGAGAGCGCATGCTCTGCGCATCTGTAGGCGCATCCGCTGTGTAAGGCTTCCGC 3050
Qy 297 IlePheIysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSer 316
Db 3051 ATCTTCAAGCTGTGCGCCCACTCCAGAGGCGCTGAGATCCTCGGCGCAACGCTGAGGCG 3110
Qy 317 CysAlaSerGluLeuGlyPheLeuLeuPheSerIleuThrMetAlaIleIleIlePheAla 336
Db 3111 TCCATGCGGAGCGGAGATGCTCATCTTCTTATATGAGGCTCATCTTTTCTCC 3170
Qy 337 ThrValMetPheTyrAlaGluLysGlySerSerAlaSerIlyPheThrSerIleProAla 356
Db 3171 AGCGCGGCTACTTGTCCGAGGAGACAGACCCCACTTCAAGTTTCAGAGATCCCGAT 3230
Qy 357 SerPheTyrTyrThrIleValIleThrMetThrThrLeuGlyTyrGlyAspMetValProIys 376
Db 3231 GCCTTCTGTGTGGAGGTGTAAACATGACACAGTGGGTACGCGGATATACACCCAGTG 3290
Qy 377 ThrIleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValIleValIleAla 396
Db 3291 ACCATAGGGGGCAAGATTGTGGATCTCTGTGCCATCTCCGCGGTCTTACCATTCGCA 3350
Qy 397 LeuProValIleProValIleValIleSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAla 416
Db 3351 TTGGCAGTTCCCGATTTGTTTCCAACTTCAATTACTTTCACACCGGAGACAGAAAGG 3410
Qy 417 AspLysArgArg-----AlaGlnLysLysAla 425
Db 3411 GAAGAGCAATCCAGTACATGACGTCGGAAATTGCCAGCACCTTCTTTCAGCCGAG 3470

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Qy 426 ArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAlaTyrLeuHisSerLys 445
Db 3471 GAGCTCCGAAAGAGAGAGAACTGACTGTGATGATGCGAGTATATGATGATGAA 3530
Qy 446 ArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457
Db 3531 GAGGGGGGTATGAACTACGAGCTTTCGCCAGACC 3566

RESULT 14
US-09-949-016-324
; Sequence 324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-324

Alignment Scores:
Pred. No.: 2,81e-61 Length: 3004
Score: 712.50 Matches: 167
Percent Similarity: 53.46% Conservative: 96
Best Local Similarity: 33.94% Mismatches: 160
Query Match: 20.88% Gaps: 69
DB: 12

US-10-062-879-2 (1-655) x US-09-949-016-324 (1-3004)
Qy 18 GlyTyrPheProValAlaAsnCys-----PrometPro 28
Db 138 GGGGCCCCGCTCAAGCGGCGCTGTGGCGGCGGCGCTGCCAGCCGCTACGAGCCGCTGCG 197
Qy 29 -----LeuAlaProAlaAspLysAsnLysArgGlnAspGluLeuIleValLeuAsnVal 46
Db 198 CCCTCATGCGCGGCGGCGGCGGAGAGACGTCGCGGAGCGCGGTGATCATCATC 257
Qy 47 SerIlyArgArgPheGlnThrTyrPArgThrThrLeuGluArgTyrProAspThrLeuLeu 66
Db 258 TCCGCGCTGTGCTTCCGAGCGAGCTGAGACCTTTCGCAAGCTTCCGAGAGCGCTCTG 317
Qy 67 GlySerThrGluLysGluPhe-----PhePheAsnGluAspThrLysGluTyrPhePheAsp 85
Db 318 GGGCAACCCCAAGCGCGCATGAGTACTTCAACCGCTCCGCAACGAGTACTTTTTCGAC 377
Qy 86 ArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr---GlyLysLeuHis 104
Db 378 CGCAACGCGCGCGAGCTTTCGAGCGCATCTCTACTACTATCATGTCGCGGCGCGCATCCGC 437
Qy 105 TyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPheTyrGlyIleLeu 124
Db 438 CGGCGGCTGCAACGCGCCATCGACATTTCTCCGAGAGATCCGCTTCTACAG----- 491
Qy 125 ProGluIleIleGlyAspCysCysTyrGluGluTyrIlyAspArgLysArgGluAsnAla 144
Db 492 -----CTGGCGAGAGGCGCATGAGAAATTCCGCGAG----- 524
Qy 145 GluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSerMetProSerLeuSer 164

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Db      525 -----GACGAGGGCTTCGTGGGAGGAGGAGGCGGCGCTTGCCCGCCGCGGAC 572
Qy      165 PheArgIntrMecTTPaRgAlaPheGluAenProHsrThrSerThrLeuAlaLeuVal 184
Db      573 TTTCCAGCGCCAGGTGGCTGCTCTTCCTCGAAGTACCAGACCTCCGGGCGGCGGAGCG 632
Qy      185 PheYrTyRValThnglyPhePheIleAlaValSerValIleThraAnValValGluThr 204
Db      633 ATGCCCATCGTGTCCGCTGCTGTCATCTCTCAATCTCAATGTATGATCTTCTGCTGAAGCG 692
Qy      205 ValProCysGlyThrValProGlySerIlySGluLeuProCys----- 218
Db      693 CTGGCG-----GAGTTCGGGAGAGAAAGGACATACCCCGCTCGACGTGCAGAGCTCA 746
Qy      219 -----GlyGluArg-----TyrSerVal 224
Db      747 TTCGAGCAGCGCGGCAACGACGTCGGGGTCCGCGGAGAGGCTCCAGCTTCGCGCAT 806
Qy      225 AlaPhePheCysLeuAapThrAlaCysValMetIlePheThrValGluTyRLeuLeuArg 244
Db      807 CCTTCTTTCGTGGTGGAGACGCTGTGATCATCTGTGTTCTCTTCCGAATCTGTGTGGCG 866
Qy      245 LeuPheAlaAlaProSerArgTyRArgPheIleArgSerValMetSerIleIleAapVal 264
Db      867 TTCCTCGCTGTTCCTAGCAAAAGCACCCTTTCGGAAACATCAATGACCTGATGCACATT 926
Qy      265 ValAlaIleMetProTyRTrpIleGlyLeuValMet-----Thr 277
Db      927 GTGGCGCATCATCTCTTATTTATCACTCTGGGTACCGAGCTGGCGCAACGACGGCAT 986
Qy      278 AenAenGluAapValSerGlyValAPheVal---ThrLeuArgValPheArgValPheArg 296
Db      987 GGACAGCGCGGCATGTCTCTGGCCATCTTGAGGGTCACTCGCTGTGAAGGGTCTTCGCG 1046
Qy      297 IlePheIysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyRThrLeuIysSer 316
Db      1047 ATCTTCMAAGCTGTGGCGGCACTCCAGAGGGGTGCAGACCTCTGGGCAAAAGCTGAAGCG 1106
Qy      317 CysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAla 336
Db      1107 TCCATGCGCGGAGCTGGAGTGTCTCATCTTCTTCCTTATGGGGGTCACTCTTTCCTCC 1166
Qy      337 ThrValMetPheTyRAlaGluIlySerIleSerAlaSerIysPheThrSerIleProAla 356
Db      1167 AGCGGCGTCTACTTTCGCGAGGACAGACCCCACTTACGTTTCAGAGCATCCGGAT 1226
Qy      357 SerPheTrpTyRThrIleValIleThrMetThrThrLeuGlyTyRGlYAspMetValProIys 376
Db      1227 GCCTTCTGTGGCGAGCTGTAAACATGACACAGAGGGTTACCGCGAATATGACACCGAGTG 1286
Qy      377 ThrIleAlaGlyIlySerIlePheGlySerIleCysSerLeuSerGlyValIleuValIleAla 396
Db      1287 ACCATAGGGGCGAAGATATTGGGATCTCTGTGTGCATCGCGCGGTCTTGACCATCGCA 1346
Qy      397 LeuProValProValIleValIleSerAsnPheSerArgIleTyRHisGlnAsnGlnArgAla 416
Db      1347 TTGCGCATGTCCCGGTGATGTTTCCAACTTCAATTACTTTCACACCGGGAGACAGAAAGG 1406
Qy      417 AspIlyAspArg-----AlaGlnIlyIlyAla 425
Db      1407 GAAGAGCATCCCACTATCATGCACTGGGAAGTTCACGACACTCTCTCTTCAGCGGAG 1466
Qy      426 ArgIleuAlaArgIleArgValAlaIleYThrGlySerSerAsnAlaTyRLeuHisSerIys 445
Db      1467 GAGCTCCGAAAGACAAAGATTAACTCGACTGTAGTAAGTGGAGTATATGCTGATCGAA 1526
Qy      446 ArgAenGlyIleLeuAsnGlnAlaIleuGluLeuThr 457
Db      1527 GAGGGGGGTATGAACATATGCGCTTTCGCCACGAGACC 1562

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Patient No. 5827655
GENERAL INFORMATION:
APPLICANT: Chandry, Kanianbhara G.
APPLICANT: Canalan, Michael D.
APPLICANT: Grissmer, Stephan
APPLICANT: Goldin, Alan L.
APPLICANT: Dethlefs, Brent A.
APPLICANT: Gutman, George A.
APPLICANT: Masmuth, John J.
TITLE OF INVENTION: Assay, Methods and Products Based On n
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Flehr, Hohbach, Test, Albritton & Herbert,
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/527,152
FILING DATE: UNKNOWN
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/170,418
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,568
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-54444-2/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1994 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 150..1736
US-08-527-152-1
Alignment Scores:
Pred. No.: 1,57e-61 Length: 1994
Score: 712.00 Matches: 175
Percent Similarity: 50.64 Conservative: 104
Best Local Similarity: 31.76 Mismatches: 197
Query Match: 20.87 Indels: 76
DB: 1 Gaps: 12
US-10-062-879-2 (1-655) x US-08-527-152-1 (1-1994)
Oy 4 G|YValAlAAlATrPheuProPhheaIlaRgaIaaIaaIalleglYTrPmetProVaIaIa 23
Db 166 GGAGACCACTGCTGGAGCGCAGAGCCGCGGAGAGCGCGTGGCGGGGAC-CGCCCTCAAGGA 224
Oy 24 AsnQVS-----PrometPro----- 28
Db 225 GGCTGTGGCAGTGCGCGCGCGCGTGCAGACCGCTACGAGCACACTGSCACCGCGC 284
Oy 29 LeuaIaPrOhIaApIlyYaSnIlyArGlInaepGIuLeuIIeVallIeaSrVaIselrcly 48

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Db 285 CTGCCCGCCGCGGAGCAAGTTCCTCGCGGAGCGTGTGATCATCAACATCTCCGG 344

Qy 49 ArgArgPheGlnThrTyrArgThrThrLeuGluArgTyrProAspThrLeuLeuGlySer 68

Db 345 CTGCGCTCGAGACCGAGCTCAAGACCTCTCGCAGTTCGCCGAGACACTGCTGGGGAC 404

Qy 69 ThrGluLysGluPhe---PhePheGlnLysPheThrLysGluTyrPhePheAspArg 87

Db 405 CCCAAGCCGCGCATGCGGTACTTTGACCCCACTCCGCAATGATGATCTTCGACCGCAAC 464

Qy 88 ProGluValPheArgCysValLeuAsnPheTyrArgThr---GlyLysLeuHisTyrPro 106

Db 465 CGACCCAGCTTGAGCGCCATCTCTACTACTACAGTCCGGGGGCGCATTCGCCGCGCG 524

Qy 107 ArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPheTyrGlyIleLeuProGlu 126

Db 525 GTCAACGTCCCATCATGACATCTTCTCCAGAGATCCGCTTTACCA----- 572

Qy 127 IleIleGlyAspCysSerTyrGluGluTyrLysAspArgLysArgGluAsnAlaGluArg 146

Db 573 ---CTGGGGAGAGAGCCATGAAAGATTCCCGTAG----- 605

Qy 147 LeuMetAspAspAsnAspSerGluAsnAngInGluSerMetProSerLeuSerPheArg 166

Db 606 -----GAGGAGGGCTTCTCGCGGAGAGAGACGACCCCTGCCCGCGTGAATTCCAG 659

Qy 167 GlnThrMetTyrArgAlaPheGluAsnProHisThrSerThrLeuAlaLeuValPheTyr 186

Db 660 CGCCAGGTGGCTGCTCTTCGAATATCCGAGAGCTCCGGCGCGCCGCGGAGCATTCGC 719

Qy 187 TyrValThrGlyPhePheIleAlaValSerValIleThrAsnValAlaGluThrValPro 206

Db 720 ATTGTGTGAGTGTGGTATCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 779

Qy 207 CysGlyThrValProGlySerLysGluLeuProCys----- 218

Db 780 -----GAGTTTCGCGAGTAGAAGACTATCCGCTCCCGTCGAGAGACGTGTTGAG 833

Qy 219 -----GlyGluArgTyrSerValAlaPhe 226

Db 834 GCTGCCAACACAGACAGCTCGGGGCCCCCTTCGAGACCTCCAGCTTCTCGACCCCTTC 893

Qy 227 PheCysLeuAspThrAlaCysValMetIlePheThrValGluTyrLeuLeuArgLeuPhe 246

Db 894 TTCGTGTGTGAGAACCTGTGTGATCATCTGTGTTCTCTTGAGCTTCGTGGCGGTTCTTT 953

Qy 247 AlaAlaProSerArgTyrArgPheIleArgSerValMetSerIleIleAspValAla 266

Db 954 GCTTCCCCCAGTAAAGCCACCTTTCACAAATATCATGAACCTGATAGCATTTGGGCC 1011

Qy 267 IleMetProTyrTyrIleGlyLeuValMet-----ThrAsnAsn 279

Db 1014 ATCATTTCTTATTTTATCACTGTGGCACTGAGCTGAGCTGCAAGCAGACAGGTAAATGGCAG 1077

Qy 280 GluAspValSerGlyAlaPheVal---ThrLeuArgValPheArgValPheArgIlePhe 298

Db 1074 CAGGCGATCTGCTGCGCATCTCTAAGAGTACCTCCGCTTAGAGGATTTTCCGCACTTC 113

Qy 299 LysPheSerArgHisSerGlnGlyLeuArgGlyLeuGlyTyrThrLeuLysSerCysAla 318

Db 1134 AAGCTCTCCCGCATTTCTAAGGGGGCGAGATCTCTAGACAGACGCTGAAGGCTTCCATG 119

Qy 319 SerGluLeuGlyPheLeuAspSerLeuThrMetAlaIleIleIlePheAlaThrVal 338

Db 1194 CGGAGAGCTGGGGCTGTCAATTTCTTCTTCATTTGGGGTCACTTTTCTCAAGTCA 125

Qy 339 MetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProLasePhe 358

Db 1254 GCTTACTTTCGTGAGGACAGACGACCTTCTTGCGGTATTAAACGATATCCCGATGCTTC 131

Qy 359 TrrTyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIle 378

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Db      1314  TGGTGGGAGTAGTAAACCATATACAAACTGGTGGTATGGTATGATATGACACCCAGTACCATTA 13173
Qy      379   AlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuPro 398
Db      1374  GGAGGCAAGATATGGTGGGCTCTCTTGTGGCCATCCAGGTGTCTTGACCATTTGCATTGGCA 14330
Qy      399   ValProValIleValIserPheSerPheSerArgIleTyrHisGlnIleAsnGlnArgAlaAspLys 418
Db      1434  GTTCCCTGATGTGTTTCCAACTTAACCTACTTTCACACCGGAGACAGAAAGGGAGAG 14930
Qy      419   ArgArg-----AlaGlnLysValAlaArgLeu 427
Db      1494  CAAGCCCAAGTACATGCACGTGGGAGATGCCAGACCTCTCTCTTCCAGCCGAGAGAGCTC 15550
Qy      428   AlaArgIleArgValAlaIalysTyrGlySerSerAsnAlaTyrLeuHisSerLysArgAsn 447
Db      1554  CGAAAGCCCGGAGTAATCCATCCATCTGATGTAGTCGGAGGTATATGGATGATCGAAGAGGG 161330
Qy      448   GlyLeuLeuAsnGlnAlaLeuGlnLeuTyrGlyTyrProGlnGlnGlnIleMetGlyLys 467
Db      1614  GGTATGAAACCAAGACCGCC-----TTCGCCGAGACCCCTTCGAAGCGGCACTCCACA 16670
Qy      468   ThrTyrSerLeuIleGlnSerGlnHisHisIleLeuHisIscysLeuGlnLysTyrThr 487
Db      1668  GCCACTTGCACCAACGAAACATTAACCCCACTCTCTGTGTCAATCAAGAAATTTCACT 17270
Qy      488   GlyLeuSerTyrLeuValAlaAspAspProLeuLeu 498
Db      1728  GATGTCTAATATATGATATGATCGTGTCCAAATTCG 1760

RESULT 16
US-10-162-012-7
; Sequence 7, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Imaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,291

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US-10-062-879-2 (1-655) x US-09-949-016-1250 (1-3186)

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QY 621 -ProAlaLeuThrProGluGluSerArgProPro----- 632  
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US-09-949-016-325  
Sequence 325, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTNER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 325  
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ORGANISM: Human  
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Score: 697.50 Matches: 202  
Percent Similarity: 43.99% Conservative: 98  
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Query Match: 20.44% Indels: 171  
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Db      2784  AACAGCAATGTCAACAGATGAAACAGAGCCCTATCGAGTCTTGCGTCC-----  2834
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RESULT 19
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; Sequence 9, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:
; APPLICANT: Chandu, Kananthara G.
; APPLICANT: Kalman, Katalin
; APPLICANT: Chandu, Gritscha
; APPLICANT: Gutman, George A.
; TITLE OF INVENTION: A NO. 5559009el Voltage-Gated Potassium Channel
; NUMBER OF INVENTIONS: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Teet, Albritton & Herbert,
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431

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; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1599
; US-08-288-405A-9
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; Alignment Scores:
; Pred. No.: 4,49e-60 Length: 1599
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; Query Match: 20.40% Indels: 76
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 13, 2005, 10:33:33 ; Search time 6505.35 Seconds

(without alignments)  
4878.777 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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11: gb\_sts :  
12: gb\_sy :  
13: gb\_un :  
14: gb\_vi :

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	3403	99.7	1968	9	AF205857 Homo sapi
4	3403	99.7	2072	6	A85166 Sequence 3

5	3403	99.7	2072	6	AR204885	AR204885 Sequence
6	3397	99.6	1968	10	AF334791	AF334791 Rattus no
7	3396	99.5	1968	10	AB003587	AB003587 Rattus no
8	3395	99.5	1968	9	AF048713	AF048713 Homo sapi
9	3395	99.5	2722	9	AF120491	AF120491 Homo sapi
10	3390	99.4	1968	10	AF107781	AF107781 Homo sapi
11	3381	99.1	1968	4	AF198445	AF198445 Oryctolag
12	3381	99.1	2041	9	AF187963	AF187963 Homo sapi
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18	3284.5	96.3	1996	10	RNTU5448	U75448 Rattus norv
19	3283.5	96.2	1911	9	AF048712	AF048712 Homo sapi
20	3278.5	96.1	1911	10	AF107782	AF107782 Mus muscu
21	3277.5	96.1	17258	10	RND42975	U42975 Rattus norv
22	3269.5	95.8	2104	6	AF187964	AF187964 Homo sapi
23	3265.5	95.7	2104	6	A85168	A85168 Sequence 5
24	3265.5	95.7	2104	6	AR204886	AR204886 Sequence
25	3237.5	94.9	1977	5	AF209722	AF209722 Gallus ga
26	3035.5	89.0	4262	10	RATKV43R	L48619 Rattus norv
27	2942.5	86.2	2840	5	XLU89265	U89265 Xenopus lae
28	2853.5	83.6	1665	4	AF493549	AF493549 Oryctolag
29	2570.5	75.3	3056	5	BC045304	BC045304 Danio rer
30	2510.5	73.6	2918	4	AY147192	AY147192 Muscetele p
31	2504.5	73.4	1893	10	AF107780	AF107780 Mus muscu
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35	2498.5	73.2	2351	9	HSABJ10969	AB010969 Homo sapi
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37	2498.5	73.2	5333	5	AB028967	AB028967 Homo sapi
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39	2490.5	73.0	1893	9	AF121104	AF121104 Homo sapi
40	2474	72.5	2248	10	RATCKSA	M59980 Rat voltage
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44	2113	61.9	2646	9	AF166003	AF166003 Homo sapi
45	2113	61.9	3139	9	HSAB05898	AB05898 Homo sapi

## ALIGNMENTS

RESULT 1	AR371346	Sequence 1 from patent US 6395477.	2121 bp	DNA	linear	PAT 12-SEP-2003
LOCUS	AR371346					
DEFINITION	Sequence 1 from patent US 6395477.					
ACCESSION	AR371346					
VERSION	AR371346.1	GI:34608278				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 2121)					
AUTHORS	Cockett,M.I., Dilks,D.W., Ling,H.-P.C. and Sokol,P.T.					
TITLE	Human potassium channel polynucleotide and polypeptides and uses thereof					
JOURNAL	Patent: US 6395477-A 1 28-MAY-2002;					
FEATURES	source	Location/Qualifiers				
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Alignment Scores:			
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Score:	3412.00	Matches:	655
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-062-879-2 (1-655) x AR371346 (1-2121)

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QY 21 ProValAlaAsnCyProMetProLeuAlaProAlaAspIlyAsnIyAsnIyArgIAsnGlu 40

Db 133 CCGGTGGCCAACTGGCCCATGCGCTGGCCCGGGCCGACAGAAACAGGCGGAGTGGAG 192

QY 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrThrArgThrThrLeuGluArg 60

Db 193 CTGATTGCTCTCAACGAGTGGGCGGAGGTTCCAGACCTGGAGAGCACGCTGGAGCGCC 252

QY 61 TyrProAspThrLeuLeuGlySerThrGluIyPhePhePheAsnGluAspThrIlyS 80

Db 253 TACCCGGACACCTGCTGGGCGACACGAGAAAGAGTCTTCTTCAACGAGACACCAAG 312

QY 81 GluIyTrPhePheAspArgAspProGluValPheArgCyValLeuAsnPheTrArgThr 100

Db 313 GAGTACTTCTTCCACCGGAGACCCCGAGTGTTCGGCTGGCGCTCAACTTCTACCGCAG 372

QY 101 GlyIyLeuHisTrpProArgTrgIuCySileSerAlaThrAspAspGluLeuAlaPhe 120

Db 373 GGGAGCTGACATACCCGCGCTACGAGTGCATCTGCTTACGACACAGAGCTGGCTTC 432

QY 121 TyrGlyIleLeuProGluIleIleGlyAspCySeyTrgIuGluIyTrIyAspArgIlyS 140

Db 433 TACGGCATCTTCCCGGAGATCATCGGGGACCTGCTGCACGAGAGATACAAAGACCGCAAG 492

QY 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGluIySerMet 160

Db 493 AGGAGAAACCCCGAGCGGCTCATGACGACAAACAGACTCGGAGAAACACGAGGTCCAG 552

QY 161 ProSerIySerPheAspArgIuThrMetThrArgAlaPheGluAsnProIlySerThr 180

Db 553 CCTCGCTGACCTTCCGACACCATGTGGCGGCTTCGAGAAACCCACACACACAGCAG 612

QY 181 LeuAlaLeuValPheTrgIyValIleThrGlyPhePheIleAlaValSerValIleThrAsn 200

Db 613 CTGGCCCTGGTCTTCTACATGAGTGCAGTGGCTTCTTACATCGCTTCTCGGATCACCAAC 672

QY 201 ValValGluThrValProCySgIyThrValProGlySerIySgIuLeuProCySgIyGlu 220

Db 673 GTGGTGAAGACGGGCGGTGCGGACCGGTCCCGGCGAGCAAGAGCTGGCGGGGAG 732

QY 221 ArgTrgSerValAlaPhePheCySleuAspThrAlaCySValMetIlePheThrValGlu 240

Db 733 CGTACTCGGTGGGCTTCTTCTGCTGGACACGCGGTGATGATCTTACCGGTGAG 792

QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTrgPheIleArgSerValIleMetSer 260

Db 793 TACCTCTGGGCTCTTCTGGGCTCCGACCGCTACCGCTTCTCCGACGCTACGAGC 852

QY 261 IleIleAspValValAlaIleMetProTrgTrgIyIleGlyLeuValMetThrAsnAsnGlu 280

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QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheIyS 300

Db 913 GAGGTGTCGGGCGCTTCTGACGCTCGGCTCTTCCGCTTTCAGGATCTTCAAGTTT 972

QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyIyTrgThrLeuIySerCySAlaSerGlu 320

Db 973 TCCCGCACACTCCAGGCGCTGCGGATCTGGGCTACACATGAAAGCTTGCTCGCA 1032

QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThrValIleMetPhe 340

Db 1033 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092

QY 341 TyrAlaGluIySgIySerSerAlaSerIyPhePheThrSerIleProAlaSerPheTrpIy 360

Db 1093 TATCCGAGAAAGGCTCTCGGCGACAGAGTTCAACAGATCCCTGCTGTTTGGTAC 1152

QY 361 ThrIleValThrMetThrThrLeuGlyIyTrgIyAspMetValProIyThrIleAlaGly 380

Db 1153 ACCATTGTCACTAGACACACTGGATACGAGACATGTGTGCTTAAGATGTGACAGG 1212

QY 381 LysIlePheGlySerIleCySerLeuSerGlyValLeuValIleAlaLeuProValPro 400

Db 1213 AAGATCTTGGCTCATCTGCTCTTGAAGTGGCTCTGATGCTTGGCTTGGCCAGTCCCT 1272

QY 401 ValIleValSerAsnPheSerArgIleTyTrhIleGlnAsnGluArgAlaAspIyAspArg 420

Db 1273 GTGATTGTTTCACTTATGCCGGAATTACACACAGATCAGAGAGCTGATTAACGAGG 1332

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Db 1333 GCACAAAGAGAGCCCGCTTGGCAGAGATCCGTGTGGCCAAACAGGACATTCGAATGCA 1392

QY 441 TyrLeuHisSerIyAspAsnGlyIyLeuLeuAsnGluAlaLeuGluIyLeuThrGlyThrPro 460

Db 1393 TACCTGCACAGACAGCGCAAGGCTCTTCAACGAGGCGCTGGAGCTGACGCGGACCCCA 1452

QY 461 GluGluGluHisMetGlyIyThrThrSerLeuIleGluSerGlnHisHisIleLeuLeu 480

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Db 1513 CACTGCTGGAAGAAACCACTGGGTGTCTTATCTTGTGATGATCCCTGTTATCTGTA 1572

QY 501 ArgThrSerThrIleIyAsnHisGluPheIleAspGluIlePheGluIyAsnCyS 520

Db 1573 CGAACCTTCACATCAAGAACACAGAGTTATGTATGATGAGAGATGTTGAGCAGAACTGC 1632

QY 521 MetGluSerSerMetGlnAsnTrgProSerThrArgSerProSerLeuSerSerHisPro 540

Db 1633 ATGAGAGTTCAATGCAAGATCACTACCAAGAGTCCCTCACTGTCAGGCAACCA 1692

QY 541 GlyLeuThrThrThrCySeySerArgSerIyIyIyThrThrHisIleuProAsnSer 560

Db 1693 GGCCTCACTACCACTGCTGCTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1752

QY 561 AsnLeuProAlaThrArgLeuArgSerMetGlnIyLeuSerThrIleHisIleGlnGly 580

Db 1753 AACCTGCAGGTACTGCTGCGGACGATGCAAGAGCTGACAGATTCACATCCAGAGC 1812

QY 581 SerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuIyAlaAspAspGly 600

Db 1813 AGTGAAGACCTCTCCCTCAACAGTGCCTCCAGCTTAAATTTGAAGACAGAGCGA 1872

QY 601 LeuArgProAsnCyIyThrSerGlnIleThrThrAlaIleIleSerIleProThrPro 620

Db 1873 CTGAGACCAAACTGCAAAACATCCAGATCCACACAGCATCATCATCATCCACATCCC 1932

QY 621 ProAlaLeuThrProGluGlyIySerArgProProProAlaSerProGlyProAsnThr 640

Db 1933 CCAGCGCTAACCCAGAGGGGAAAGTCGGCACCCCTGACACCCAGAGGCCCAACAGC 1992

QY 641 AsnIleProSerIleThrSerAsnValIyIyValSerValIySerValIySerValIy 660

Db 1993 AACATTCTTCAATACAGCAATGTGTCAAGGTCTGTCTTG 2037

RESULT 2

AX956786 1968 bp DNA linear PAT 08-JAN-2004

LOCUS AX956786

DEFINITION Sequence 4 from Patent WO03097682.

ACCESSION AX956786

VERSION AX956786.1 GI:40785267

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.





[illegible]

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QY	41	Leu11Leu	Val	Leu	Asn	Val	Ser	Gly	Val	Arg	Val	Phe	Gln	Thr	Trp	Arg	Thr	Thr	Leu	60			
DB	121	CTGATGTCTCTCA	ACG	TAG	TGG	GGC	CGG	AGG	TTT	CC	AG	CTT	CAAC	CG	AG	CA	CG	AG	CA	180			
QY	61	Tyr	Trp	Asp	Thr	Leu	Leu	Gly	Ser	Thr	Gln	Val	Phe	Gln	Phe	Asn	Gln	Val	Asp	Thr	80		
DB	181	TACCCGGA	CAAC	CCCT	CGT	CGG	CAG	CA	CGG	AA	AGG	AGT	TTT	CTT	CAAC	CG	AG	CA	CG	AG	240		
QY	81	Glu	Val	Trp	Phe	Asp	Asp	Arg	Pro	Glu	Val	Phe	Arg	Cys	Val	Leu	Asn	Phe	Tyr	Arg	Thr	100	
DB	241	GAGTAC	TTCTT	CCAC	CGG	GAC	CCCG	AG	AGT	GTG	TCC	GT	CGT	CGT	CTC	CA	ACTT	CT	CA	CG	AG	300	
QY	101	Gly	Val	Leu	His	Arg	Tyr	Pro	Arg	Tyr	Glu	Cys	Ala	Ser	Ala	Tyr	Asp	Asp	Glu	Leu	Ala	Phe	120
DB	301	GGGAAG	CTG	CA	CTAC	CCG	CGT	AG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	360
QY	121	Tyr	Gly	Val	Leu	Pro	Gln	Val	Leu	Arg	Cys	Val	Arg	Gln	Val	Arg	Val	Arg	Val	Arg	Val	140	
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QY	141	Arg	Glu	Asn	Ala	Arg	Leu	Met	Asp	Asp	Asn	Asp	Ser	Glu	Asn	Arg	Gln	Val	Ser	Met	160		
DB	421	AGGGAAGA	ACG	CGA	CGG	CTC	AT	TGA	CGA	CA	CGA	CT	CGA	GA	AA	CA	CGA	CGA	CGA	CGA	CGA	480	
QY	161	Pro	Ser	Leu	Ser	Phe	Arg	Gln	Thr	Met	Trp	Arg	Ala	Phe	Gln	Val	Asn	Pro	His	Ser	Thr	180	
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QY	181	Leu	Ala	Leu	Val	Phe	Tyr	Tyr	Val	Thr	Gly	Phe	Met	Leu	Ala	Val	Ser	Val	Leu	Thr	Asn	200	
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QY	261	Leu	Leu	Asp	Val	Val	Ala	Leu	Met	Pro	Tyr	Tyr	Leu	Gly	Leu	Val	Met	Thr	Asn	Asn	Glu	280	
DB	781	ATCATCG	ACG	GGT	GGC	AT	CAT	AT	CC	TAC	AT	CA	TG	CGT	CGT	CA	TG	CA	CA	CA	CA	CA	840
QY	281	Asp	Val	Ser	Gly	Ala	Phe	Val	Thr	Leu	Arg	Val	Phe	Arg	Val	Phe	Arg	Val	Phe	Phe	Phe	300	
DB	841	GACGTG	TCCG	CGCTT	CGT	CA	CGCT	CCG	GGT	CTT	CCG	CGT	CTT	CA	GA	AT	CTT	CA	GA	AT	CTT	900	
QY	301	Ser	Trp	His	Ser	Gln	Gly	Leu	Arg	Leu	Gly	Tyr	Thr	Leu	Ser	Ser	Cys	Ala	Ser	Glu	320		
DB	901	TCCGCA	CACTCC	CA	GGG	CTG	CGG	AT	CTT	GGG	CTT	CA	CT	GA	AG	AG	AG	AG	AG	AG	AG	960	
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QY	341	Tyr	Ala	Gly	Ser	Gly	Ser	Ser	Ala	Ser	Val	Phe	Thr	Ser	Leu	Pro	Ala	Ser	Phe	Trp	Tyr	360	
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RESULT 4  
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DEFINITION Sequence 3 from Patent WO9842833.  
ACCESSION A85166  
VERSION A85166.1 GI:6733868  
KEYWORDS  
ORGANISM  
SOURCE unidentified  
unclassified.  
REFERENCE  
1. (bases 1 to 2072)  
AUTHORS Britl A.M. and Calmels T.P.  
TITLE KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  
JOURNAL Patent: WO 9842833-A 3 01-Oct-1998;  
BRIT ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)  
FEATURES  
source 1..2072

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Score: 3403.00 Matches: 653  
Percent Similarity: 99.69% Conservative: 0  
Best Local Similarity: 99.69% Mismatches: 2  
Query Match: 99.74% Indels: 0  
DB: Gaps: 0  
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| | | | |  
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 Rattus.  
 REFERENCE 1 (bases 1 to 1968)  
 AUTHORS Song, M., Helguera, G., Eghbali, M., Zhu, N., Zarei, M.M., Olcese, R.,  
 Toro, L. and Stefani, E.  
 TITLE Remodeling of Kv4.3 potassium channel gene expression under the  
 JOURNAL control of sex hormones  
 MEDLINE J. Biol. Chem. 276 (34), 31883-31890 (2001)  
 PUBMED 21402960  
 11427525  
 REFERENCE 2 (bases 1 to 1968)  
 AUTHORS Eghbali, M., Zhu, N., Toro, L. and Stefani, E.  
 TITLE Direct Substitution  
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KEYWORDS Ky4.3.  
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ORGANISM Rattus norvegicus, Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (sites)  
AUTHORS Ohwa, S., Tanaka, M., Oku, T., Asai, Y., Matanabe, M., Giles, W.R. and Imaizumi, Y.  
TITLE Molecular cloning and tissue distribution of an alternatively spliced variant of an A-type K<sup>+</sup> channel alpha-subunit, Kv4.3 in the rat  
JOURNAL FEBS Lett. 420 (1), 47-53 (1997)  
MEDLINE 98111009  
PubMed 9450548  
REFERENCE 2 (bases 1 to 1968)  
AUTHORS Imaizumi, Y.  
TITLE Direct Submission  
JOURNAL Submitted (06-MAY-1997) Yoji Imaizumi, Nagoya City University, Pharmacology and Therapeutics; 3-1 Tanabe-dori, Mizuho-ku, Nagoya, Aichi 467, Japan (E-mail: yimaizumi@phar.nagoya-cu.ac.jp, Tel: 052-836-3433, Fax: 052-836-3432)  
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 Qy 581 SerGluInProSerleuThrThrSerArgSerSerleuAsnleuValAspAspGly 600  
 Db 1741 AGTGAAGAGCGCTCTCCACAAACAGTGTGCTCAGGCTTATTTGAAGAAGACGACGGA 1800

Qy 601 leuArgProAsnGlylyThrSerGlnleThrThrAlailelleSerilleProThrPro 620  
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 long splice variant, complete cds.  
 ACCESSION AF120491  
 VERSION AF120491.1 GI:5059059  
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 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 2722)  
 Iebbrandt, D., Leicher, T., Wajdschütz, R., Zhu, X., Lühmann, U.,  
 Michel, U., Sauter, K. and Pongs, O.  
 Gene structures and expression profiles of three human KCND (Kv4)  
 potassium channels mediating A-type currents I(70) and I(SA)  
 Genomics 64 (2), 144-154 (2000)  
 JOURNAL MEDLINE  
 PUBMED 20195625  
 10729221  
 2 (bases 1 to 2722)  
 REFERENCE Zhu, X.R., Wajdschütz, R., Iebbrandt, D., Sauter, K. and Pongs, O.  
 Direct Submision  
 Submitted (15-JAN-1999) ZMNH, Institut fuer Neuraale  
 Signalverarbeitung, Martinstrasse 52, Hamburg 20246, Germany  
 JOURNAL  
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 Pred. No.: 6,49e-223 Length: 2722  
 Score: 3395.00 Matches: 653  
 Percent Similarity: 99.69% Conservative: 0



Best Local Similarity: 99.69%  
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US-10-062-879-2 (1-655) x AF120491 (1-2722)

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 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murine; Mus.  
 REFERENCE 1 (bases 1 to 1968)  
 AUTHORS Tanaka,H., Janzen,K., Winkfein,R.J., Fiset,C., Clark,R.B. and Giles,W.R.  
 TITLE Cloning and functional characterization of mouse heart K+ channel alpha subunits, Kv1.5, Kv4.2 and Kv4.3  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1968)  
 AUTHORS Tanaka,H., Janzen,K., Winkfein,R.J., Fiset,C., Clark,R.B. and Giles,W.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-NOV-1998) Physiology and Biophysics, University of Calgary, 3330 Hospital Dr. NW, Calgary, AB T2N 1N4, Canada  
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ORIGIN

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US-10-062-879-2 (1-655) x AF107781 (1-1968)

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 REFERENCE  
 1 (bases 1 to 2041)  
 Dिल्के,D., Ling,H.P., Cockett,M., Sokol,P. and Numann,R.  
 Cloning and expression of the human Kv4.3 potassium channel  
 J. Neurophysiol. 81 (4), 1974-1977 (1999)  
 MEDLINE  
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 PUBMED  
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 REFERENCE  
 2 (bases 1 to 2041)  
 Dिल्के,D.W., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.  
 Direct Submission  
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REFERENCE  
1 (bases 1 to 2057)  
Patel,S.P., Campbell,D.L., Morales,M.J. and Strauss,H.C.  
Heterogeneous expression of Kchir2 isoforms in the ferret heart  
J. Physiol. (Lond.) 539 (Pt 3), 649-656 (2002)

JOURNAL  
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PubMed  
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REFERENCE  
2 (bases 1 to 2057)  
Patel,S.P., Morales,M.J. and Strauss,H.C.  
Direct Submission  
Submitted (03-DEC-2001) Physiology and Biophysics, University at  
Buffalo-SUNY, 3435 Main Street, 124 Sherman Hall, Buffalo, NY  
14214, USA

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AUTHORS	Cockett,M.I., Dlike,D.W., Ling,H.-P.C. and Sokol,P.T.		
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Qy	261	IleIleAspValValAlaIleMetProTyrrTyrrIleGlyLeuValMetThrAsnAsnGlu	280
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Qy	281	AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheIysPhe	300
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Db	1093	TATCCCGAAGAGGCTCTCGGCGCAGAGATTCACAAGCATCCCTGCTGTTTGGATC	1152
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 VERSION AF205856.1 GI:6644149  
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 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 AUTHORS Calmeis,T.P.G., Faivre,J.-F., Javre,J.-L., Cheval,B., Rouanet,S.  
 and Brill,A.

TITLE Long and Short Human Isoforms of the Kv4.3 Channel: Cloning,  
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 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1911)  
 AUTHORS Calmeis,T.P.G., Faivre,J.-F., Javre,J.-L. and Brill,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-1999) Cardiovascular Pharmacology, Smithkline  
 Beecham, 4 Rue du Chesnay Beauregard, Saint Gregoire 35760, France  
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Pred. No.: 5e-216 Length: 1911  
 Score: 3291.50 Matches: 634  
 Percent Similarity: 96.79% Conservative: 0  
 Best Local Similarity: 96.79% Mismatches: 2  
 Query Match: 96.47% Indels: 19  
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US-10-062-879-2 (1-655) x AF205856 (1-1911)

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 AUTHORS Brill,A.M. and Calmels,T.P.  
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 JOURNAL  
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DEFINITION Sequence 1 from patent US 6368823.
ACCESSION AR204884
VERSION AR204884.1 GI:21502324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2104)
AUTHORS Brill,A.Michel,Alain., Calmele,T.Paul.Gerard.,
FAIVRE,J.-F.,Simon,Pierre., Javre,J.-L. and Rouanez,S.
TITLE kv potasium channel polypeptides and polynucleotides
JOURNAL Patent: US 6368823-A 1 09-APR-2002;
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Alignment Scores: 5.68e-216 Length: 2104
Pred. No.:

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US-10-062-879-2 (1-655) x AR204884 (1-2104)

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Dp	301	GGGAAAGCTGACATACCGGGCTACGAGTGCATCTTGGCTTCAGACAGACACTGGCTTC	360
OY	121	TyrGlyLleuLeuProGluLleIleGlyAspCysCysTyrGluGluTyrLysAspArgLys	140
Dp	361	TACGGCATCTCCCGAGAGTCACTCGGGAGCTGCTCTAGAGAGTACAAAGACCGAG	420
OY	141	ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnLysMet	160
Dp	421	AGGAGAAACCCGAGCGGCTCATGAGACAAACGACTGGAGAACACAGAGATCCATG	480
OY	161	ProSerLleuSerPheArgGlnThrMetTPArgAlaAPheGluAsnProHisThrSerThr	180
Dp	481	CCCTCGCTCAAGTTCGGCCAGACAGTGGGGGCTTCGAGAACCCCAACACAGACAG	540
OY	181	LeuAlaLeuValPheTyrTyrValAThrGlyPhePheIleAlaValSerValIleThrAsn	200
Dp	541	CTGGCCTGGTCTTACTACAGTGACTGGCTCTTCAATCGCTGTCCGTATACACAC	600
OY	201	ValValGluThrValProCysGlyThrValAProGlySerLysGluLeuProCysGlyGlu	220
Dp	601	GTGGTGGAGACGGAGCGGTGGCAGCGTCCGGGGAGGACAGAGACTCGGTGGGGAG	660
OY	221	ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu	240
Dp	661	CGCTAATCGGTGGCTTCTTCTGCTCGGACAGCGGGGTGGTCAATCTTCAACGTTGAG	720
OY	241	TyrLleuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer	260
Dp	721	TACTCTCTGGGCTCTTCCGGGCTCCAGACCGCTACCGCTTCAATCCGAGGCTATAGC	780
OY	261	IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu	280
Dp	781	ATCATCGACGGTGGGCATCATGCCCTACTACATGAGGTCTGTATGACCAACACAG	840
OY	281	AspValSerGlyValAPheValAThrLeuArgValAPheArgValAPheArgIlePheLysPhe	300
Dp	841	GACCTGTCCGGCGCTTCGACAGCTCCGGGCTTCCGGGTTCAGAGATCTTCAAGTTT	900
OY	301	SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLleuLysSerCysAlaSerGlu	320
Dp	901	TCCGGCACTCCAGGGGCTCGGAGTCTTGAGGCTACACACTAAGAGCTGTGCTCCGA	960
OY	321	LeuLysPheLeuLeuPheSerLleuThrMetAlaIleIlePheAlaThrValMetPhe	340

Db	961	CTGGGGCTTTCTTCTCTCTCCCTCACCATGGCCATCATCTTTGGCACTGGATGTTT	1020
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Qy	361	ThrLleValThmMetThrThrLleuGlyTYrGlyAspMetValProLYsTrpLleAlaGly	380
Db	1081	ACCAATTCTCACATGACACACTGGGATACGAGACATGGTGCCCTTAGACATTTGCAGGG	1140
Qy	381	LYsLlePheGlySerLleCYsSerSerLeuSerGlyValLleuValLleAlaLeuProValPro	400
Db	1141	AAAGTCTTCGGCTCCATCTGCTCTTGAAGTGGGCTGCTGGTCAATTGGCCCGCAAGTCCCT	1200
Qy	401	ValLleValSerAnPheSerArgLleTYrThiGlnAsnGlnArgAlaAspLYsArgArg	420
Db	1201	GTGATGTTTTCAAACTTTTACCCGGATTTTACACACAGATCAGAGAGCTGTAAACGACAG	1260
Qy	421	AlaGlnLYsLYsAlaArgLleuAlaArgLYsValAlaLYsThrArgLYsSerSerAsnAla	440
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Qy	441	TYrLeuHisSerLYsArgAnGlyLleLleLeuAsnGlnValaLeuGlnLeuThrGlyThrPro	460
Db	1321	TACTTGACACAGCAAGCCCAAGGGCTCTCTCAAGAGGCGGTGGAGCTGACAGGGACCCCA	1380
Qy	461	GluGluGluLuhISMetGlyLYsThrThrSerLleuLleGluSerGlnHisSHISLleuLeu	480
Db	1381	GAAGAAGAGACATAGGGCAGAACACCTCTCATCAGAGCCAGCATCATCACTCTCTG	1440
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Qy	501	ArgThrSerThrLleLYsAsnHisGluPheLleAspGluGlnMetPheGlnGlnAsnCYs	520
Db	1462	-----AACCAAGATTATTATGATAGACAGATGTTTGAGACAGAACTGC	1503
Qy	521	MetGluSerSerMetGlnAsnTYrProSerThrArgSerProSerLeuSerSerHisPro	540
Db	1504	ATGAGAGATTCAATAGCAAGAACTACCATCCACAAAGAAAGTCCCTCATCTGCACGACCCCA	1563
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RWU75448 RWU75448 1996 bp mRNA linear ROD 05-NOV-1996			
DEFINITION Rattus norvegicus Kv4.3 potassium channel mRNA, complete cds.			
ACCESSION U75448.1 GI:1658482			
VERSION			

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 1996)  
Dixon, J.E., Shi, W., Wang, H.S., McDonald, C., Yu, H., Wymore, R.S.,  
Cohen, I.S., and McKinnon, D.  
Role of the Kv4.3 K<sup>+</sup> channel in ventricular muscle. A molecular  
correlate for the transient outward current  
Circ. Res. 79 (4), 659-668 (1996)  
96428386  
8831489  
2 (bases 1 to 1996)  
Dixon, J.E., Shi, W., and McKinnon, D.  
Direct Submission  
Submitted (18-OCT-1996) Neurobiology, SUNY at Stony Brook, Life  
Sciences Building, Stony Brook, NY 11794-5230, USA  
Location/Qualifiers  
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ORIGIN

Alignment Scores:  
Pred. No.: 1.6e-215 Length: 1996  
Score: 3284.50 Matches: 633  
Percent Similarity: 96.79% Conservative: 1  
Best Local Similarity: 96.64% Mismatches: 2  
Query Match: 96.26% Indels: 19  
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US-10-062-879-2 (1-655) x RNUT5448 (1-1996)

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QY 161 ProSerLeuSerPheArgGlnThrMetTyrPheAlaPheGlnAaenProHisTyrSerThr 180  
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 Db 1813 AGTAGAGAGCCCTCTCTCCACACAGATCGCTCCAGCTTATTTGAAAGCAGACGACGGA 1872  
 Qy 601 LeuArgProAsnCysLysThrSerGlnLleThrThrAlaLleLleSerLleProThrPro 620  
 Db 1873 CTGAGACCAAACTGCAAAACATCCCAAGTACCAAGCATCATCATCAGATCCCACTCCC 1932  
 Qy 621 ProAlaLeuThrProGlnGlnGlyGluSerArgProProAlaSerProGlyProAsnThr 640  
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 DT 26-FEB-2004 (first entry)  
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 XX  
 KW Antiarhythmic; cardiovascular; anticonvulsant; cerebroprotective;  
 KW tranquilliser; sedative; neuroprotective; nootropic; antiparkinsonian;  
 KW nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;  
 KW blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;  
 KW tachycardia; congestive heart failure; epilepsy; stroke;  
 KW traumatic brain injury; anxiety; insomnia; Alzheimer's disease;  
 KW Parkinson's disease; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
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 PD 27-NOV-2003.  
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 PF 14-MAY-2003; 2003WO-IB002453.  
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 PR 15-MAY-2002; 2002US-0378076P.  
 PR 15-MAY-2002; 2002US-0378131P.  
 XX  
 PA (DEVG-) DEVGEN NV.  
 XX  
 PI Kaletta TJ, Dewulf NE, Plaetinck GKM;  
 XX  
 DR WPI, 2004-061981/06.  
 DR P-PSDB; ADF91398.  
 XX  
 PT New nematode worm expressing a heterologous nucleotide sequence encoding  
 PT a functional voltage-gated potassium channel of the Kv4 family, useful  
 PT for determining compounds that interact with the voltage-gated potassium

PT channel.  
 XX  
 PS Example 1; SEQ ID NO 4; 82pp; English.  
 XX  
 CC The invention relates to a nematode worm that expresses a heterologous  
 CC nucleotide sequence encoding a functional voltage-gated potassium channel  
 CC of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,  
 CC part or fragment. The nematode worm is useful in determining whether a  
 CC compound interacts with the voltage-gated potassium channel of the Kv4  
 CC family or whether a compound is an agonist, antagonist, opener and/or  
 CC blocker of the voltage-gated potassium channel expressed by the nematode  
 CC worm. The methods are used for identifying and developing compounds that  
 CC interact with voltage-gated potassium channels of the Kv4 family. The  
 CC compounds may be used in the development and/or preparation of  
 CC compositions for pharmaceutical, agrochemical and/or veterinary use.  
 CC These may be used in preparing compositions for preventing or treating  
 CC diseases or conditions such as arrhythmia, tachycardia, congestive heart  
 CC failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,  
 CC Alzheimer's disease or Parkinson's disease. The current sequence  
 CC represents wild-type hkv4.3 cDNA.  
 XX  
 SQ Sequence 1968 BP; 426 A; 648 C; 511 G; 383 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3,94e-276 Length: 1968  
 Score: 3403.00 Matches: 653  
 Percent Similarity: 99.69% Conservative: 0  
 Best Local Similarity: 99.69% Mismatches: 2  
 Query Match: 99.74% Indels: 0  
 DB: Gaps: 0  
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 Qy 41 LeuLleValLeuAsnValSerGlyArgArgPheGlnThrTyrArgThrLysLeuArg 60  
 Db 121 CTGATTTCTTCAACGTAATGGGCGGAGTTCCAGACTGAGGAGCAACGCTGAGACGC 180  
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 DB 1621 GGCTCTACATCACTGCTGCTCCGCTCGTATGTAAGACACACACCTGCGCCATTTCT 1680  
 QY 561 AsnLeuProAlaThrArgLeuArgSerMetGlnIleLeuSerThrIleHisIleGlnGly 580

DB 1661 AACCTGCAGTACTCTCCCTGGCAGCATCAAGAGCTTACAGCAAGATCCATCCAGGCG 1740  
 QY 581 SerGlnIleProSerLeuThrThrSerArgSerSerLeuAsnLeuValAlaAspArgIle 600  
 DB 1741 AGTAGACAGCCCTCTCCCTCAACACAGTCCCTTCAAGCTTATTTGAAGACAGACGGA 1800  
 QY 601 LeuArgProAsnCysIleThrSerGlnIleThrThrAlaIleIleSerIleProThrPro 620  
 DB 1801 CTGAGACCAAACTCAAAACATCCCAAGATCAACACACCATCATCATGACATCCCACTCCC 1860  
 QY 621 ProAlaLeuThrProGlnGlyIleValArgProProAlaSerProGlyProAsnThr 640  
 DB 1861 CCAGGCTTAACCCCAAGAGGAGAAAGTCGGCCACCTTCCAGCCCAAGGCCCCCAACAG 1920  
 QY 641 AsnIleProSerIleThrSerAsnValValIleValSerValLeu 655  
 DB 1921 AACATCTCTTCCATAGCCAGCAATGTGTCAAGGTCTCCGCTTG 1965  
 RESULT 3  
 AAV61572 ID AAV61572 standard; cDNA; 2072 BP.  
 AC AAV61572;  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Human Kv potassium channel hKv4.3 (longer isoform) cDNA.  
 KW Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
 KW therapy; diagnosis; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1965  
 FT /\*tag= a  
 PN W09842833-A2.  
 XX  
 PD 01-OCT-1998.  
 XX  
 PF 23-MAR-1998; 98WO-EP001901.  
 XX  
 PR 27-MAR-1997; 97GB-00006377.  
 PR 09-DEC-1997; 97EP-00402971.  
 PR 11-DEC-1997; 97EP-00403007.  
 XX  
 PA (SMIT) SMITHKLINE BEECHAM LAB PHARM.  
 XX  
 PI Bril ANA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;  
 DR MPI: 1998-542277/46.  
 DR P-PSDB; AAW79590.  
 XX  
 PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding  
 PT poly:nucleotide(s) useful in the treatment of disorders including cardiac  
 PT arrhythmias and Alzheimer's disease.  
 XX  
 PS Claim 2; Page 26; 47pp; English.  
 XX  
 CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see  
 CC AAW79590). It shows about 92% identity in 1932 nucleotides to rat Kv4.3.  
 CC A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated  
 CC from human heart cDNA by PCR amplification (see AAV61574-77). Another  
 CC claimed polynucleotide (see AAV61571) encodes an isoform (see AAW79589)  
 CC of hKv4.3 having 19 fewer amino acid residues. The invention relates to  
 CC these hKv4.3 polynucleotides and polypeptides and to methods for  
 CC producing such polypeptides by recombinant techniques. Also claimed are  
 CC methods for utilising the hKv4.3 polynucleotides for the treatment of  
 CC subjects in need of enhanced or reduced activity or expression of hKv4.3  
 CC polypeptide. These include the treatment of cardiac arrhythmias and  
 CC Alzheimer's disease. The invention can also be used to identify agonists

CC and antagonists of hKv4.3, and to detect disease associated with  
CC inappropriate hKv4.3 expression or activity

XX Sequence 2072 BP; 449 A; 681 C; 541 G; 401 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	4,24e-276	Length:	2072
Score:	3403.00	Matches:	653
Percent Similarity:	99.69%	Conservative:	0
Best Local Similarity:	99.69%	Mismatches:	2
Query Match:	99.74%	Indels:	0
DB:	2	Gaps:	0

US-10-062-879-2 (1-655) x AAV61572 (1-2072)

QY 1 MetAlaAaGlyValAlaAlaTPrLeuProPheAlaArgAlaAlaAlaIleGlyTyrMet 20  
Db 1 ATGGCGGACAGAGATTGGACGGCTGCTCTTTGCGGGCTGCGGCATGCGGTGATG 60  
QY 21 ProValAlaAaenCySPromerProLeuAlaProAlaAplysAaenlySAArgGlnAspGlu 40  
Db 61 CCGGTGGCCAACTGCCCCATGCCCCCTGACCCGGCCGACAAAGAAAGCGGACGATGAG 120  
QY 41 IleuIleValIleuAenValSerGlyArgArgPheGlnThrTPArgThrThrLeuGlnArg 60  
Db 121 CTGATTGTCTCAACGTAAGTGGGCGAGGTTCCAGACCTGAGAGACCAAGCTGGAGCC 180  
QY 61 TyrProAspThrLeuLeuGlySerThrGlnulysGlnPhePhePheAaenGlnAspThrLys 80  
Db 181 TACCCGAGACCCCTGCTGGGACAGAGAAAGAGTTCTTCTTCAAGAGACCAAG 240  
QY 81 GluTyrPhePheAspArgAspProGlnuValPheArgCysValIleuAaenPheTyrArgThr 100  
Db 241 GAGTACTTCTTCGACCGGAGACCCGAGAGTGTTCGCTGCGCTCAACCTTCTTACCGCAG 300  
QY 101 GlyLysLeuHisTyrProArgTyrGlnCysIleSerAlaTyrAspAspGlnLeuAlaPhe 120  
Db 301 GGGAGCTGCACACCCGCGCTACGAGTGCATCTCTGCTTACGACGAGAGCTGGCTTC 360  
QY 121 TyrGlyIleLeuProGlnuIleIleGlyAspCysCysTyrGlnuGlnuTyrLysAspArgLys 140  
Db 361 TACGGACTCTCCCGGAGATCATCGGGAGCTGTCTTACGAGAGTCAAGACCGCAG 420  
QY 141 ArgGlnAaenAlaGlnuGleuMetAspAspAaenAspSerGlnuAaenGlnuIleSerMet 160  
Db 421 AGGAGAAACCGCGAGCTCATGAGACAAACACTCGAGAAACAACGAGACTCCATG 480  
QY 161 ProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGlnuAaenProHisSerThr 180  
Db 481 CCTCGCTCAGCTTCCGACAGACCATGTGGCGGCTTCAAGAACCCCAACACAGACG 540  
QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaIleSerValIleThrAsn 200  
Db 541 CTGGCCCTGGGCTTCTTACAGTACGTGGCTTTCATCGCTGTCTGGTATCAACCAAC 600  
QY 201 ValValGlnThrValProCysGlyThrValProGlySerLysGlnuLeuProCysGlyGln 220  
Db 601 GTGGTGAGACGGGTGGCGGACGAGTCCCGGCGACAAAGGAGCTGCGTGGGGAG 660  
QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
Db 661 CGCTACTCGGGGCTTCTTCTGCTGAGACAGCGGCGCATGATCTTACCGTGGAG 720  
QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
Db 721 TACTCTCGGGGCTTCTTCTGCGGCTCCAGCGGCTTACCGGAGGTATGATGAGC 780  
QY 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAaenGln 280  
Db 781 ATCATCAGCGGTGGCATATGCCCCATCAATCGGCTGTGTCATGACCAACAGAG 840  
QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300

Db 841 GACGTGTCGGCGCTTCTGTCAGCGCTCCGGATCTTCCGCGCTTCCAGGATCTTCAAGTTT 900  
QY 301 SerArgHisSerGlnuGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGln 320  
Db 901 TCCGCGACATCCAGAGGCTGGCGGATCTTGAGCTTACACCTGAAGACTGTGCTCCGAA 960  
QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
Db 961 CTGGGCTTCTTCTCTTCTTCTCCCTACCATGCGCATCATCTTGTGCACGTGATGTTT 1020  
QY 341 TyrAlaGlnuLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTyrTyr 360  
Db 1021 TATGCCAGAAAGGCTCTCTCGGCGACAGATTCACAAAGCATCCCTGCTGTGTGGTAC 1080  
QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGly 380  
Db 1081 ACCATTTCACCATGACACACATGGATGAGAGACATGGTGCTTACAGACATTCAGGG 1140  
QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValIleuValIleAlaLeuProValPro 400  
Db 1141 AAGATCTTCGGCTTCATCTGCTCTTGAAGGCGTCTGTGCATGTGCTGCGCAGTCCCT 1200  
QY 401 ValIleValSerAaenPheSerArgIleTyrHisGlnAaenGlnuArgAlaAplysArgArg 420  
Db 1201 GTGATTGTTCCAACTTACCGGATTTACCAACAGATCAGAGAGCTGATAACGACAG 1260  
QY 421 AlaGlnuLysValaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
Db 1261 GCACAAAGAGGCCCCCTTGGCAGGATCCGTTGGCCAAACAGGCACTTGAAGTCA 1320  
QY 441 TyrLeuHisSerLysArgAaenGlyLeuLeuAaenGlnuAlaLeuGlnuLeuThrGlyThrPro 460  
Db 1321 TACCTGACAGACAGGACCAAGGCTCTTCAAGAGGCGTGGAGCTGAGCGGACCCCA 1380  
QY 461 GlnuGlnuIleHisMetGlyLysThrThrSerLeuIleGlnuSerGlnuHisIleLeuLeu 480  
Db 1381 GAAGAGAGACATGGGCAAGACCACTCATCTATGAGAGCCAGCATCATCACTGCTG 1440  
QY 481 HisCysLeuGlnuLysThrThrGlyLysSerTyrLeuValAspAspProLeuLeuSerVal 500  
Db 1441 CACTGCTGAAAAAACACTGGGTGTCTTACTTGTGTGATGATATCCCTGTTATCTGTA 1500  
QY 501 ArgThrSerThrIleLysAaenHisGlnuPheIleAspGlnuIleMetPheGlnuAaenCys 520  
Db 1501 CGAATCTCCACATCAAGAACCAAGATTTATGATGACAGATGTTGAGCAGAACTGC 1560  
QY 521 MetGlnuSerSerMetGlnuAaenTyrProSerThrArgSerProSerLeuSerSerHisPro 540  
Db 1561 ATGGAGAGTTCATATGACGAATCCCATCCACAAGAAAGTCCCTCATGTCAGGCCCA 1620  
QY 541 GlyLeuThrThrThrCysCysSerArgArgSerLysThrThrHisLeuProAaenSer 560  
Db 1621 GGCTCACAACCACTGCTCTCCCGCTGTAAGAAAGCAACACCTGCCCAATCTT 1680  
QY 561 AsnLeuProAlaThrArgLeuArgSerMetGlnuLeuSerThrIleHisIleGlnuGly 580  
Db 1681 AACCTGCAGCTACTGCTGCGAGATGCAAGAGCTTCAGACGATCCATCCAGGGC 1740  
QY 581 SerGlnuProSerLeuThrThrThrSerArgSerSerLeuAaenLysValaAspAspGly 600  
Db 1741 AGTGAGAGGCTCTCCCTCAACACAGTCGCTCCAGGCTTAAATTGAAGACAGACGAGA 1800  
QY 601 LeuArgProAaenCysLysThrSerGlnuIleThrThrAlaIleIleSerIleProThrPro 620  
Db 1801 CTGAGACCAAACTGCAAAACATCCAGATCACCAGCCCACTCATGACATCCCACTCCC 1860  
QY 621 ProAlaLeuThrProGlnuGlyLysArgProProProAlaSerProGlyProAaenThr 640  
Db 1861 CAGCGCTTAAACCCAGAGGGGAAAGTGGGCAACCCCTTCCAGGCCCAAGCCCAACAG 1920  
QY 641 AsnIleProSerIleThrSerAaenValaLysValSerValLeu 655  
Db 1921 AACATTCCTTCCATAGCAGACATGTGTCAAGGTCTCCGCTTG 1965

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RESULT 4
ABEN84401
ID ABEN84401 standard; cDNA; 2064 BP.
XX
XX ABEN84401;
AC
XX
XX 01-OCT-2002 (first entry)
DT
XX
XX Human Kv4.3 potassium channel (short form) cDNA.
DE
XX
XX Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
KM neotropic; neuroprotective; cardiac; gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 73..1983
FT CDS /*tag= a
FT /product= "Kv4.3"
FT
XX
XX US6395477-B1.
XX
XX 28-MAY-2002.
XX
XX 23-OCT-1998; 98US-00178109.
XX
XX 23-OCT-1998; 98US-00178109.
XX
XX 23-OCT-1998; 98US-00178109.
XX
XX (AMHP ) AMERICAN HOME PROD CORP.
XX
XX
XX Cockect MI, Dicks DW, Ling HC, Sokol PT;
XX
XX WPI; 2002-556093/59.
XX
XX P-PSDB; ABB79585.
XX
XX
XX New isolated polynucleotide encoding human Kv4.3 potassium channel
PT polypeptide, useful as probe in a diagnostic method for detecting nucleic
PT acid encoding human Kv4.3, and for treating Alzheimer's and heart
PT diseases.
XX
XX
XX Claim 7; Col 21-22; 19pp; English.
XX
XX
XX The present sequence is that of cDNA encoding the short isoform of novel
CC human potassium channel Kv4.3. 2 isoforms of human Kv4.3 have been
CC identified. One form is full-length (hKv4.3 long) while the second form
CC has a deletion of 19 amino acids in the carboxy domain after the
CC predicted sixth transmembrane domain (hKv4.3 short). Human heart
CC primarily expresses hKv4.3 long, whereas human brain contains both forms.
CC To obtain the present hKv4.3 short cDNA, PCR amplification was performed
CC using primers that flanked the 57 bp insert in hKv4.3 long. The invention
CC provides Kv4.3 polypeptides, polynucleotides, and methods for producing
CC these polynucleotides. The Kv4.3 polypeptides and polynucleotides are
CC useful in the diagnosis, treatment and screening of human diseases
CC relating to an excess or deficiency of hKv4.3 activity, including
CC Alzheimer's disease and heart disease
XX
XX Sequence 2064 BP; 446 A; 678 C; 545 G; 395 T; 0 U; 0 Other;
SQ

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Alignment Scores:
Pred. No.: 1.78e-267 Length: 2064
Score: 3300.50 Matches: 636
Percent Similarity: 97.10% Conservative: 0
Best Local Similarity: 97.10% Mismatches: 0
Query Match: 96.73% Indels: 19
DB: 6 Gaps: 1

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US-10-062-879-2 (1-655) x ABEN84401 (1-2064)

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Qy 1 MetAlaIaGlyValAlaIaTrpLeuProPheAlaArgAlaAlaIaIleGlyTTrpMet 20
Db 73 ATGGCGGCGGAGTTCGGGCTGCTGCTTTTCCCGGCGGCTGCGGCATCGGTGGATG 132

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Qy 21 ProValAlaAsnCySPrometProLeuAlaProAlaAspLysAsnLysArgGluAspGlu 40
Db 133 CGGATGGGCAATGCCCCCATGCCCCCTGGCCCGGACAGAAACAAGCCGCGATGGAG 192
Qy 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrrArgThrThrLeuGluArg 60
Db 193 CTGATTTGCTTCACACGTAAGTGGGCGGAGTTCCAGACCTGGAGGACCAAGCTGGAGCGG 252
Qy 61 TyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThrLys 80
Db 253 TACCCGACACCCCTGCGGCGAGCAGCAGAGAAGAGTCTTCTTTCACACGAGGACACCAAG 312
Qy 81 GluTyrPhePheAspAspAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100
Db 313 GAGTACTTCTTCGACCGGAGACCCGAGGTGTTCCGCTGCGTCTTCATCCGACG 372
Qy 101 GlyLysLeuHisTyrProArgTyrGluCysAlaSerAlaTyrAspAspGluLeuAlaPhe 120
Db 373 GGGAAAGCTGACATACCCGCGCTAGAGTGCATCTCTGCTACGACGAGAGCTGGCTTC 432
Qy 121 TyrGlyTlleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArgLys 140
Db 433 TACGCAATCCTCCCGGAGATCATCGGAGCTGCTGTACAGAGAGTACAGAGACCGCAG 492
Qy 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnLysSerMet 160
Db 493 AGGAGAAAGCCGAGCCGCTCATGACAGACAGATCTCGAGAAACAACGAGAGTCCATG 552
Qy 161 ProSerLeuSerPheArgGlnThrMetTrrArgAlaPheGluAsnProHisThrSerThr 180
Db 553 CCTCGCTCAGCTTCCGCGAGACCATGTGGCGGGCTTCAGAAACCCCAACAGACAG 612
Qy 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200
Db 613 CTGGCCCTGCTCTTCTACTAGTACGTGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCT 672
Qy 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220
Db 673 GTGGGAGAGAGGCGGTGGGCGAGCGTCCCGGAGCAAGAGAGCTGCGTGGGAGAG 732
Qy 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240
Db 733 CGTACTCGTGGGCTTCTTCTGCTGAGACCGCGGTGCTGATGATCTTCAACGTTGAG 792
Qy 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260
Db 793 TACTCCCGCGGCTCTTCCGCGCTCCAGCGCTTCACTGCTTCACTGCTGCTGCTGCTGCT 852
Qy 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnGlu 280
Db 853 ATCATCGACGTGGTGGCCATCATGCTTACTACATCGGTGCTGATGACCAACACAGAG 912
Qy 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300
Db 913 GACGTGTCGGCGCTTCTGTCAGCTCCGGTCTTCCGCGCTTCAAGATCTTCAAGTTT 972
Qy 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320
Db 973 TCCCGCACTCCCAAGGCGCTCGGATCTCGGCTACACACAGAGAGCTGCTCCGAA 1032
Qy 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThrValMetPhe 340
Db 1033 CTGGGCTTCTTCTTCTTCTTCTTCCACCAATGCAATCACTTGTGCACTGGATGTT 1092
Qy 341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTrrPyr 360
Db 1093 TATGCCGAGAGGCTCTCTGCGCAGCAAGTTCACAGACATCCTGCTGCTGTTTGGTAC 1152
Qy 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGly 380
Db 1153 ACCATTGTACCATGACACACTGGATACGGAACATGTGGCTTAAGACGATTTGACAGGG 1212
Qy 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400

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Db      1213 AAGATCTCGGCTCATCTGCTCTGAGTGGCGTCTGCTCATTTGCCCTCCAGTCCCT
Qy      401  Val1eValSerAenPheSerArg11eTyThiSeGlnenGlnAaArg1AaArgArg
Db      1273 GTGATTTCTTCAACTTAGCGGATTTTACCAAGATCCAGAGCTGATTAACGCGAGG
Qy      421  AlaGlnIysLysAlaArgLeuAlaArg11eArgValAlaLysTrnGlySerSerAsnAla
Db      1333 GCACAAAGAAAGGCCCTTGGCAGATCCGTGTGGCCAAAGAGCGAGTTCCAAATGCA
Qy      441  TyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGlnLeuTrnGlyThrPro
Db      1393 TACCTGCACAGCAAGCCAGCGGCTCCTCAACAGAGGGCTGAGCTGACGCGACGCCCA
Qy      461  GlnGlnGlnHisMetGlyLysTrnThrSerLeu11eGlnSerGlnHisHisLeuLeu
Db      1453 GAAGAGAGAGCAAGAGGAGACCACTCACTCACTGAGACCGACATCACCCTGCTG
Qy      481  HisCysLeuGlnLysTrnThrGlyLeuSerTyrLeuValaAspAspProLeuLeuSerVal
Db      1513 CACTGCTTGAAAAAACCACT-----
Qy      501  ArgThrSerThrIleLysAsnHisGlnPhe11eAspGlnGlnMetPheGlnAsnGly
Db      1534 -----AACCAAGAGTTTATTTATGAGAGAGATGTTTGAACAGACAGTGC
Qy      521  MetGlnSerSerMetGlnAsnTrnProSerThrArgSerProSerLeuSerSerHisPro
Db      1576 ATGAGAGAGTTCAAGTCAAGAACTACCACTCCCAAGAAAGTCCCTCACTGTCAGCCACCA
Qy      541  GlnLeuThrTrnThrCysSerArgArgSerLysLysTrnHisLeuProAsnSer
Db      1636 GGCTCACTACACCTGCTGCTCCGTCGTAAGTAAGAAAGACACACCTGCCCATACTCT
Qy      561  AsnLeuProAlaThrArgLeuArgSerMetGlnLysLeuSerTrnHis11eGlnGly
Db      1696 AACCTGCAGCTATCTCCCTGCGAGCATGCAAGAGCTCAGCAAGATCCATCAGGCG
Qy      581  SerGlnGlnProSerLeuThrTrnThrSerArgSerSerLeuAsnLeuValaAspAspGly
Db      1756 AGTGAGAGAGCCCTCTCACACACAGTCGCTCCAGCTTAATTTGAAGACAGACGGA
Qy      601  LeuArgProAsnCysLysTrnSerGln11eThrTrnAla11eSer11eProThrPro
Db      1816 CTGAGACCAAACTGCAAAATCCCAATCCACATCCACAGCATCATCAGATCCCATCTCC
Qy      621  ProAlaLeuThrProGlnGlyGlnSerArgProProProAlaSerProGlyProAsnThr
Db      1876 CAGCGCTAACCCCAAGAGGGGAAAGTCGGCCACCCCTGCGACCCCAAGCCCAACAG
Qy      641  Asn11eProSer11eThrSerAsnValaValaValaSerValLeu
Db      1936 AACATTCCTTCATTAACAGCAATGTGTCAAGGTCTCTGCTGTG 1980

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XX      MO9842833-A2.
PN      01-OCT-1998.
XX      23-MAR-1998; 98WO-EP001901.
XX      27-MAR-1997; 97GB-00006377.
PR      09-DEC-1997; 97EP-00402971.
PR      11-DEC-1997; 97EP-00403007.
XX      (SMIK ) SMITHKLINE BEECHAM LAB PHARM.
PA      Bril AMA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
PI      P-PSDS; AAW79589.
DR      WPI: 1998-542277/46.
XX      New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
PT      poly:nucleotide(s) useful in the treatment of disorders including cardiac
PT      arrhythmias and Alzheimer's disease.
XX      Claim 2; Page 24; 47pp; English.
PS      This cDNA sequence codes for human Kv potassium channel hKv4.3 (see
CC      AAW79589). It shows about 92% identity in 1913 nucleotides to rat Kv4.3.
CC      A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated
CC      from human heart cDNA by PCR amplification (see AAV61574-77). Another
CC      claimed polynucleotide (see AAV61572) encodes an isoform (see AAW79590)
CC      of hKv4.3 having an additional 19 amino acids. The invention relates to
CC      these hKv4.3 polynucleotides and polypeptides and to methods for
CC      producing such polypeptides by recombinant techniques. Also claimed are
CC      methods for utilising the hKv4.3 polynucleotides for the treatment of
CC      subjects in need of enhanced or reduced activity or expression of hKv4.3
CC      polypeptide. These include the treatment of cardiac arrhythmias and
CC      Alzheimer's disease. The invention can also be used to identify agonists
CC      and antagonists of hKv4.3, and to detect disease associated with
CC      inappropriate hKv4.3 expression or activity
XX      SQ Sequence 2104 BP; 461 A; 678 C; 559 G; 406 T; 0 U; 0 Other;

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Alignment Scores:

Prod. No.:	1.05e-266	Length:	2104
Score:	3291.50	Matches:	634
Percent Similarity:	96.79%	Conservative:	0
Best Local Similarity:	96.79%	Mismatches:	2
Query Match:	96.47%	Indels:	19
DB:	2	Gaps:	1

US-10-062-879-2 (1-655) x AAV61571 (1-2104)

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Qy      1  MetAlaAlaGlyValAlaAlaTrpLeuProPheAlaArgAlaAlaAla11eGlyTrpMet
Db      1  ATGGCGGCAAGAGATGGAGCTGCTGCTTTGGCCCGGCGCTGGCCATCGGCTGATG
Qy      21  ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArgGlnAspGlu
Db      61  CCGGTGGCCAACTGCCCCCATGCCCCCTGGCCCCCGGCGCAAGAACAAAGCGAGGATGAG
Qy      41  Leu11eValLeuAsnValSerGlyArgArgPheGlnTrnTrpArgTrnThrLeuGlnArg
Db      121  CTGATTTCTTCAACGTGAGTGGCGGAGGTTCCAGACTCGAGAGACCAAGCTGAGACGC
Qy      61  TyrProAspThrLeuLeuGlnSerTrnGlnLysGlnPhePheAsnGlnAspThrLys
Db      181  TACCGGAGACCTGCTGGCGACAGCAAGAAAGAGTTCTTCAACGAGACCAACAG
Qy      81  GlnTyrPhePheAspArgAspProGlnValPheArgCysValLeuAsnPhyTrnArgThr
Db      241  GAGTACTTCTTCAACCGGAGCCCGAGGTTGCGGCTGCGGTCTCACTTACCGACG
Qy      101  GlyLysLeuHisTrpProArgTyrGlnCys11eSerAlaTrnAspAspGlnLeuAlaPhe

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RESULT 5  
AAV61571  
ID AAV61571 standard; cDNA; 2104 BP.  
XX AAV61571;  
DT 11-JAN-1999 (first entry)  
XX Human Kv potassium channel hKv4.3 (shorter isoform) cDNA.  
XX Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
KM therapy; diagnosis; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT 1..1908  
CDS /\*tag= a  
FT

Db 301 GGGAGCTGCACTACCGCGCTACAGATGATCTCTGCTACAGACAGAGCTGCGCTTC 360  
 QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGlyGluIleTyrIleAspArgIys 140  
 Db 361 TACGGCATCTCTCCCGGAGATCATCGGGGACTGCTGCTACAGAGATACAGAGCCCGCAAG 420  
 QY 141 ArgGluAsnAlaGluIleArgLeuMetLaspAsnAspSerGlyLysAsnGlnGlyIleuSerMet 160  
 Db 421 AGGAGAAAGCCGACGCGCTCATGACAGACAGACACTCGAGAAACAGAGAGTCCATG 480  
 QY 161 ProSerLeuSerPheArgGlnThrMetTyrPArgAlaPheGlyLysAsnProHisThrSerThr 180  
 Db 481 CCTCGCTCATGCTTCGCGCAGACCATGTGCGGCGCTTCGAGAAACCCACACAGACAG 540  
 QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
 Db 541 CTGGCCCTGCTCTTCTACTACGTAGCATGCGCTTCTTCACTGCTGCTGCGGATCACCAAC 600  
 QY 201 ValValGluThrValProCysGlyThrValProGlySerIleGluLeuProCysGlyGly 220  
 Db 601 GTGGTGAAGACGGTGGCGGACGGTCCGAGGACAGAGAGCTGCGCGGAG 660  
 QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
 Db 661 CGCTACTCGGTGGCTTCTTCTGCTGAGACAGCGCGCTCATGATCTTCACTGAGAG 720  
 QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
 Db 721 TACCTCTGCGGCTTCTGCGGCTCCAGCGCTTACCGCTTACCGCAGCGCATGAGAC 780  
 QY 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnGln 280  
 Db 781 ATCATTCACGGTGGGCTCATGATGCTTACTACATGCTGTGATCAGACCAACAGAG 840  
 QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheIysPhe 300  
 Db 841 GACGTGTCGGCGCTTCTGTCACCGCTCGGCTTCTGCGCTTCTGAGATCTTCAAGTTT 900  
 QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuIleSerCysAlaSerGlu 320  
 Db 901 TCCCGCCACTCCCGAGGCTGCGGATCTCTGGGCTACACATGAAAGACTGTGCTCGAA 960  
 QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
 Db 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020  
 QY 341 TyrAlaGluIleGlySerSerAlaSerIlePheThrSerIleProAlaSerPheTyrPyr 360  
 Db 1021 TATGCCAGAAAGGCTCTCTGCGCAGACAGATTCACAGATCTCTGCTGCTTGTGATC 1080  
 QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIysThrIleAlaGly 380  
 Db 1081 ACCATTTGACACATGACACACATGAGATACGAGAACTGTGCTTAAGATTTGACAGGG 1140  
 QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
 Db 1141 AAGATCTTCTGCTCATCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200  
 QY 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspIleValArg 420  
 Db 1201 GTGATGTGTTCCACTTTAGCGGATTTACACCAAGATCAGAGAGCTGATTAAGCGAGG 1260  
 QY 421 AlaGlnIleValAlaArgLeuAlaArgIleArgValAlaIleThrGlySerSerAsnAla 440  
 Db 1261 GCACAAAAGAAAGGCGCGCTTGCAGAGATCGGTGSCAAAACAGGCAATTTGAATGCA 1320  
 QY 441 TyrLeuHisSerIleValArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThrGlyThrPro 460  
 Db 1321 TACCTGACAGCAAGCGCAAGGCTCTCTCAACAGAGCGCTGAGCTGAGAGGCGACCCCA 1380  
 QY 461 GluGluGluIleHisMetGlyIleThrThrSerLeuIleGluSerGlnHisHisIleLeuLeu 480  
 Db 1381 GAAGAGGAGCACATGGGACAGACCACTCACTACAGAGCGACATCATCACTGCTG 1440

QY 481 HisCysLeuGluIleValThrThrGlyLeuSerTyrIleValAlaAspAspProLeuLeuSerVal 500  
 Db 1441 CACTGCTCGGAAAAAACCTC----- 1461  
 QY 501 ArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGluGlnAsnCys 520  
 Db 1462 -----MACCAGAGATTTATGATAGCAGATGTTTGAAGCAAGAACTGC 1503  
 QY 521 MetGluSerSerMetGlnAsnTyrProSerThrTyrArgSerProSerLeuSerSerHisPro 540  
 Db 1504 ATGAGAGATTCATAGCAGAACTACCATCCACAAAGAGTCCCTCACTGTCAGCCACCA 1563  
 QY 541 GlyLeuThrThrThrCysCysSerArgArgSerIleValThrHisIleuProAsnSer 560  
 Db 1564 GGCCTCACTACCACTCTGCTGCTCCGTCGATGAAGAAACACACACCTGCGCAATCTT 1623  
 QY 561 AsnLeuProAlaThrArgLeuArgSerMetGlnIleuSerThrIleHisIleGlnGly 580  
 Db 1624 AACCTGCCAGCTACTCGCTGCGCAGCATGCAAGAGCTCAGCAGATCCACATCCAGGCG 1683  
 QY 581 SerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAspAspGly 600  
 Db 1684 AGTGAAGAGCCCTCCTCCACAAACAGTCGCTCCAGCTTAATTTGAAGACAGACGAGA 1743  
 QY 601 LeuArgProAsnCysGlyThrSerGlnIleThrThrAlaIleIleSerIleProThrPro 620  
 Db 1744 CTGAGACCAAACTCAAAACATCCAGATCACCAAGCATCATCAGATCCCATCCCTCC 1803  
 QY 621 ProAlaLeuThrProGluGlyGluSerArgProProProAlaSerProGlyProAsnThr 640  
 Db 1804 CCAAGGCTAACCCCAAGAGGGGAAAGTCGGCCACCCCTGCGCAGCCCAAGGCCCAACAG 1863  
 QY 641 AsnIleProSerIleThrSerAsnValValIleValSerValLeu 655  
 Db 1864 AACATTCCTTCATAGCCAGCAATGTTGTCAAGGTCTCCGCTTG 1908  
 Db  
 RESULT 6  
 AA61573  
 ID AA61573 standard; cDNA; 2104 BP.  
 AC AA61573;  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Human Kv potassium channel hKv4.3 cDNA.  
 KW Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
 XX therapy; diagnosis; ss.  
 OS Homo sapiens.  
 FH  
 FT  
 FT CDS 1..1911  
 FT /\*tag= a  
 PN W09842833-A2.  
 XX  
 PD 01-OCT-1998.  
 XX  
 PF 23-MAR-1998; 98WO-EP001901.  
 XX  
 PR 27-MAR-1997; 97GB-00006377.  
 PR 09-DEC-1997; 97EP-00402971.  
 PR 11-DEC-1997; 97EP-00403007.  
 XX  
 PA (SMITK) SMITHKLINE BEECHAM LAB PHARM.  
 PI Bril AWA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;  
 XX  
 DR WPI; 1998-542277/46.  
 DR P-PSDB; AAW795591.  
 XX



PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding  
PT poly:nucleotide(s) useful in the treatment of disorders including cardiac  
arrhythmias and Alzheimer's disease.

PS Claim 18, Page 27; 47pp; English.

XX  
CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see  
CC AAW79591). It was isolated using expressed sequence tag analysis. The  
CC sequence has about 91% identity in 1914 nucleotide residues with rat  
CC Kv4.3 potassium channel. Full-length hKv4.3 cDNA clones (see AAW61571-72)  
CC are also claimed. The invention relates to hKv4.3 polynucleotides and  
CC polypeptides and to methods for producing such polypeptides by  
CC recombinant techniques. Also claimed are methods for utilizing hKv4.3  
CC polynucleotides for the treatment of subjects in need of enhanced or  
CC reduced activity or expression of hKv4.3 polypeptide. These include the  
CC treatment of cardiac arrhythmias and Alzheimer's disease. The invention  
CC can also be used to identify agonists and antagonists of hKv4.3, and to  
CC detect disease associated with inappropriate hKv4.3 expression or  
CC activity

XX  
SQ Sequence 2104 BP; 462 A; 679 C; 560 G; 403 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	1.61e-264	Length:	2104
Score:	3265.50	Matches:	630
Percent Similarity:	96.34%	Conservative:	1
Best Local Similarity:	96.18%	Mismatches:	5
Query Match:	95.71%	Indels:	19
DB:	2	Gaps:	1

US-10-062-879-2 (1-655) x AAW61573 (1-2104)

QY 1 MetAlaIaGlyValAlaIaIaTProLeuProPheAlaArgAlaAlaIleGlyTProMet 20  
Db 1 ATGGCGGAGGAGTGGACGCTGCTGCTTTGGCCGCGGCTGGCCATGAGGAGGAGTGG 60  
QY 21 ProValAlaAenCySPrometProLeuAlaProAlaAenLySAenLyAArgAlaAspGlu 40  
Db 61 CCGGTGGCCAACTGCCCATGCCCTGGCCCCGGCCGCAAGAACAGGCGGAGATGAG 120  
QY 41 LeuIleValLeuAenValSerGlyAArgAArgPheGlnThrTPaArgThrThreugluAArg 60  
Db 121 CTGATTTCTCCCAACGTGAGTGGCGGAGGTTCCAGACCTGAGAGACACCGCTGAGCGC 180  
QY 61 TyrProAspThrLeuLeuGlySerThrGluArgGluPhePhePheAsnGluAspThrLys 80  
Db 181 TACCCGACACCTGCTGGGACGACGAGAGAGATTCTTCTTCAAGAGAGACACCAAG 240  
QY 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100  
Db 241 GAGTACTTCTTCACCGGAGCCGAGGAGTTCGCTGCGTCCAGCTCAACCTTACCGCAGC 300  
QY 101 GlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
Db 301 GGGAGAGCTGACCTACAGCGCTTACGAGTGCATCTCTGCTTACGAGAGAGCTGGCTTC 360  
QY 121 TyrGlyIleLeuProGluIleIleGlyAAspCysTyrGluGluTyrLysAspArgLys 140  
Db 361 TACGGCATCTCTCCGAGATCATCGGGCATCTGCTTACGAGAGTACAGAGACCGCAG 420  
QY 141 ArgGluAsnAlaGluAArgLeuMetAspAsnAspSerGluAsnAsnGluGluSerMet 160  
Db 421 AGGAGAGACCGGAGGAGCTATGAGACACAGATCTGGAGAACACAGAGATCCATG 480  
QY 161 ProSerLeuSerPheArgGlnThrMetTPaArgAlaPheGluAsnProHisThrSerThr 180  
Db 481 CCTCGCTCAGCTTCCGCGACACCATGAGCGGCTTCAGAGAACCCCAACACGACGACG 540  
QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
Db 541 CTGGCCCTGGTCTTCTTACTAGCTGAGCTGGCTTTCATCGCTGCTCGGTATACCAAC 600  
QY 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220

Db 601 GTGGTGAAGACGGGCGGTGGGACCGTCCCGGCGACAGAGAGCTGCGTGGGGAG 660  
QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
Db 661 CGTACTCGGGGCTTCTTCTGCTGAGACGGGCGGTGCGTCAATGATCTTACCGTGGAG 720  
QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrAArgPheIleArgSerValMetSer 260  
Db 721 TACTCTCGGGGCTTCTTCTGCGGCTCCAGCGGATCAGGCTTCACTCCGAGGCTATGAGC 780  
QY 261 IleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
Db 781 ATCATCACGCGGTGGCATATGCTTACTACATCGCTTGGTCATAGACCAACAGCAG 840  
QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
Db 841 GACGTGCGCGGCTTGTGTCACGCTCGGGTCTTCCGCGTTCAGAGATTCACAGTTT 900  
QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320  
Db 901 TCCCGCACTCCCAAGGCTGCGGATCTGGGCTACACATGAGAGACTGTGCTCCGAA 960  
QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
Db 961 CTGGGCTTTCTTCTTCTTCTTCCCTCACATGCGCATCATCTTTCACACTGTGATGTTT 1020  
QY 341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheThrTyr 360  
Db 1021 TATGCCAGAAAGGCTCTCGGCCAGAGTTCAAGATCCTCGCTGCTTGTGGTAC 1080  
QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAAspMetValProLysThrIleAlaGly 380  
Db 1081 ACCATTGTACATGACACATCTGGATACGAGACATGTGCTTAAGACATTTGACAGG 1140  
QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
Db 1141 AAGATCTTGGCTCATCTGCTCTTGAGTGGCGTCTGATTCATTCCTGCGCTGAGTCCCT 1200  
QY 401 ValIleValSerAnPheSerArgIleTyrHisGluAsnGlnAArgAlaAspLysAArg 420  
Db 1201 GTGATTTGTTCCAACTTTAGCGGATTTTACCACCAAGAAAGAGCTGATTAAGCGAGG 1260  
QY 421 AlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
Db 1261 GCACAAAGAAAGGCCCGCTTGCAGATCCGTGTGCCAAAGACGACAGTTCGAATGCA 1320  
QY 441 TyrLeuHisSerLysAArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThrGlyThrPro 460  
Db 1321 TACCTGACAGCAAGCGCAACGGGCTCTCAACAGAGCGCTGAGCTGACGCGCACCCCA 1380  
QY 461 GluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHisIleLeuLeu 480  
Db 1381 GAAGAGGAGACATGGGCAAGACCACTCATCTACAGAGCCGACATCATCACTCTG 1440  
QY 481 HisCysLeuGluLysThrThrGlyLeuSerTyrLeuValAspAspProLeuLeuSerVal 500  
Db 1441 CACTGCTCGAAGAAACACT----- 1461  
QY 501 ArgThrSerThrIleLysAsnHisGluPheIleAspGluGluMetPheGluGluAsnCys 520  
Db 1462 -----AACCAAGATTATTGATAGGACGATGTTGAGCAGAACTGC 1503  
QY 521 MetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSerSerHisPro 540  
Db 1504 ATGAGAGATTCAATGAGAACTACCCATTCACAAAGATCCCTCATCTGTCAGGCAACCA 1563  
QY 541 GlyLeuThrThrThrCysSerArgArgSerLysLysThrThrHisLysProAsnSer 560  
Db 1564 GGCTTCACTACCACTCTGCTCCGCTGTAAGTAAGAACACACACCTGCCAATTCT 1623  
QY 561 AsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHisIleGlnGly 580



Db 1624 AACCTGCCAGCTACTGCGCTGGCAGCATGCAAGAGCTCAGCATCCATCCAGGAGC 1683  
 QY 581 SerGIuGIuProSerIeuThrThrSerArgSerSerLeuAsnLeuValAlaAspAspGIY 600  
 Db 1684 AGGAGACAGCCCTCCCTCACAACCACTCCCTCAGCTTAATTGTAAGACACAGACGGA 1743  
 QY 601 LeuArgProAsnCysValSerThrSerGIuIleThrThrAlaIleIleSerIleProThrPro 620  
 Db 1744 CTGAGACCAAACTGCAAAACATCCAGATCACACAGCATCATCGCATYCCCTCC 1803  
 QY 621 ProAlaIleuThrProGIuGIuSerArgProProProAlaSerProGIuProAsnThr 640  
 Db 1804 CCAAGCGTAAACCCCAAGAGGAGGAGAGTGGGCAACCCCTGCGACAGCCCAAGGCCCAACAG 1863  
 QY 641 AsnIleProSerIleThrSerAsnValValIysValSerValIleu 655  
 Db 1864 AACATTCTTCCTCATACGACCAACGTTGTCAAGTCTCCGCGCTTG 1908

RESULT 7  
 AAH21247  
 ID AAH21247 standard; cDNA; 2351 BP.  
 XX  
 AC AAH21247;  
 DT 13-SEP-2001 (first entry)  
 XX  
 DE Human Kv4.2 cDNA.  
 XX  
 KM Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;  
 KM neurodegenerative disease; ischemia; stroke; Alzheimer's disease;  
 KM Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;  
 KM learning capacity; protein kinase activator; anti-arrhythmic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 433..2322  
 FT /\*tag= a  
 FT /product= "Kv4.2 alpha subunit"  
 XX  
 DN DEL19963612-A1.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PD 29-DEC-1999; 99DE-01063612.  
 XX  
 PR 29-DEC-1999; 99DE-01063612.  
 XX  
 PA (GENE-) FORSCHUNGSGEBELLSCHAFT GENION MBH.  
 XX  
 DR WPI; 2001-42637/46.  
 XX  
 DR P-PSDB; AAB86319.  
 PT New potassium channel subunit proteins, useful for identifying and  
 PT testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological  
 PT agents.  
 XX  
 PS Claim 11; Page 18-21; 50pp; German.  
 XX  
 CC This invention describes a novel potassium channel protein (I) that is  
 CC either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium  
 CC channels containing (I) are used to identify and test: (i) compounds for  
 CC treatment of neurodegenerative diseases (autism, epilepsy, ischemia,  
 CC stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac  
 CC arrhythmia, or those that improve learning capacity and memory; and (ii)  
 CC activators of protein kinases. Host cells that express (I) can identify  
 CC agents that do not interact significantly with channels and control I<sub>to</sub>  
 CC (a quickly activated transient current), so lack the side effects of  
 CC known anti-arrhythmic agents. They also eliminate, or reduce, the need  
 CC for testing on organ cultures  
 XX  
 SQ Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6.57e-200 Length: 2351  
 Score: 2498.50 Matches: 486  
 Percent Similarity: 84.09% Conservative: 69  
 Best Local Similarity: 73.64% Mismatches: 70  
 Query Match: 73.23% Indels: 35  
 DB: 4 Gaps: 7

US-10-062-879-2 (1-655) x AAH21247 (1-2351)

QY 1 MetAlaIaGIuValAlaIaATrPleuProPheAlaArgAlaAlaIleGIYTrMet 20  
 Db 430 ATGGAGGGGGGGGGGGGAGGAGGCTGCTGCTTTTGCAAGGCAAGCGCTATCGGAGTGA 489  
 QY 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg--GlnAsp 39  
 Db 490 CTTGTGGCTTCGGGGGCTATGCGGGCTCCCGGAGGAGAGAGAAAGAACCAAGAT 549  
 QY 40 GIuLeuIleValLeuAsnValSerGIYArgArgPheGIuThrTrpArgThrTrpLeuGIu 59  
 Db 550 GCTCTCATGTGTGTAATGTAGTGGACCGGCTTCCAGACGTGGCAGACACCTGGAA 609  
 QY 60 ArgTYrProAspThrLeuLeuGIYSerThrGIuGIuPhePhePheAsnGIuAspThr 79  
 Db 610 CATTACCAAGACACTCTACTGGGAGTTCGAGAGGAGACTTTTCTTACCAACCAAGAACT 669  
 QY 80 LysGIuTYrPhePheAspArgAspProGIuValPheArgCysValLeuAsnPheTYrArg 99  
 Db 670 CAGCAGATATTTCTTTGACCGGTGACCCAGACATCTTCGCGACATCTCGAATTTCTACCGC 729  
 QY 100 ThrGIYLysLeuHisTYrProArgTYrGIuCylSerAlaTYrAspAspGIuLeuAla 119  
 Db 730 ACTGGAGAGCTCCACTCTCCGCGACAGAGTCTCTCTTACATGATGATGAAGAACTGGCC 789  
 QY 120 PheTYrGIYLeuLeuProGIuIleIleGIYAspCysCysTYrGIuGIuTYrLysAspArg 139  
 Db 790 TTTCTTGGCTTCATCCCGGAATATCGGCAGCTGCTGTTATGAGAGATCAAGATCGC 849  
 QY 140 LysArgGIuAsnAlaGIuArgLeuMetAspAspAsnAspSerGIuAsnAsnGIuSer 159  
 Db 850 AGCGAGAGAGAACCGCGAGCGCTGCAGAGACGAGCGGATACCGACCGCTGGGAGAGC 909  
 QY 160 ---MetProSerLeuSerPheArgGIuThrMetTrpArgAlaPheGIuAsnProHisThr 178  
 Db 910 GCCTTGCCCAACAGACTGCAAGGACAGAGGCTCGAGGGCTTCGAGAACCCCAACACC 969  
 QY 179 SerThrLeuAlaLeuValPheTYrTYrValThrGIYphePheIleAlaIleSerValIle 198  
 Db 970 AGCAGATGGCCCTGGTGTCTTACTATGTCAAGGGATTTTTCATTGCGCGCTGTGTATC 1029  
 QY 199 ThrAsnValAlaGIuThrValProCysGIYThrValProGIYSer---LysGIuLeuPro 217  
 Db 1030 GCGAATGTGTGAAAGAGTCCGTCGGATCAAGCCCAAGTCAATTAAAGAACTGCC 1089  
 QY 218 CysGIYGIuArgTYrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db 1090 TGTGGAGAGCGGTATGCTGTGCTCTTCTGTGTGACACGGGCTTCGATGATCTTC 1149  
 QY 238 ThrValGIYTrpLeuArgLeuPheAlaIaIaProSerArgTYrArgPheIleArgSer 257  
 Db 1150 ACAGTGTGATATTGCTTCCTGCGCTGCGTGCAGCGCTGATGCTTATGCTTTGCGGATG 1209  
 QY 258 ValMetSerIleIleAspValAlaIaIleMetProTYrTYrIleGIYLeuValMetThr 277  
 Db 1210 GTTCATGATATCATCGACGTGTGGCATCTGCTTATTAATGTGGGCTGTGATGACA 1269  
 QY 278 AsnAsnGIuAspValSerGIYAlaPheValThrLeuArgValPheArgValPheArgIle 297  
 Db 1270 GACATGTAGGAGCGTACGGGAGCTTGTCTCACTCGAGCTTCGGGCTTACAGATC 1329  
 QY 298 PheLysPheSerArgHisSerGIuGIYLeuArgIleGIYTrpTrpLeuLysSerCys 317  
 Db 1330 TTTAAGTTTCCCGCACTTCAGAGCGCTGCGATCTTGGGGTACACACTGAAAGATTGT 1389

QY	318	AlAsersgIuLeuGIgIlyPheueuuehserLeuThrmcAlaIleIleIlePhehAlathr	337
Db	1390	GcCTCAgAAntTGGGcCTTCTGCTTTTCGCTCAcCAAGcTATATCATCTTCCCTACA	1449
QY	338	ValMetPheTyAlAGIuLyseGIySeSerAlaserIlySpherThSerIleProAlaser	357
Db	1450	GTTATGTTCTACGACAGAGAGGGGCTTCGGCTACAGATTACACAGATCCCTGACACC	1509
QY	358	PheTPrTyTThrIleValThrmcThrThrLeuGIyTyTGIyAspMetValProLyThr	377
Db	1510	TTCTGGTATACCATGTCATGCATCAACATGACACTGAGGTATGTGACATGGTGCAGAAAACC	1568
QY	378	IleAlAGIyLyseIlePheGIySerIleCySeSerIleuSerGIyValLeuValIleAlaLeu	397
Db	1570	ATAGCAGGAGAAATTTTGGTTCTTCTCTATCTGTTGCTGAGTGGGGGTCTTGATCTTCCTTA	1628
QY	398	ProValProValIleValSerAnbPheSerArgIleTyRHIsGInAsnGIaRgAlaAp	417
Db	1630	CCTGTTCGGGTGATGTATTCACAATTCATGTCATCTACACACAGAACTCAAGACGACAGAC	1689
QY	418	LybAtgAtgAlaGInLyseValAargLeuAlaArgIleAlaGValAlaLyseThGIySer	437
Db	1690	AAACCAAGAGGACAGAAAGAAAGCTGACTGGCGCAGAAATCCGGCGACCAAAAGCGAGAAC	1749
QY	438	SerAsnAlaTyRLeuHISerIlyAspRgAsnGIyLeuAsnGIaAlaLeuGIuLeuThr	457
Db	1750	GCAAAATGCTTATCATCAAGCAAGCAAGAGATGGTTACTCAAGTAACTAGCTGAG--TCC	1806
QY	458	GIyThrProGIuGIuGIuHISmetGIyThrThrThrSerLeuIleGIuSerGIuHIS	477
Db	1807	TCAGAGANTGAGCAGAGCCTTTTGTGACAAATCCGGCTCAGCTTGGAACCGACAGCAC	1866
QY	478	HisLeuLeuHISCySeLeuGIuLySThrThrGIyLeuSerTyRLeuValAspAspProLeu	497
Db	1867	CACCTGCTTCACTGCTGCGAAAAAACCGC-----	1896
QY	498	LeuSerValArgThSerThrIleLybAsnHISGIuPheIleAspGIuGIuMetPheGIu	517
Db	1897	-----AATCAcGAGTTTGTGGAGCAACAAAGTCTTGAA	1929
QY	518	GIuAsnCyMetGIuSerSerMetGIuAsnTyRProSerThrArgSerProSerLeuSer	537
Db	1930	GAAAGCTGCATGGAAGTTGCAACGTGTATGCTCTTCAAGTACAGTCTTCACTGCT	1989
QY	538	SerHisPProGIyLeuThrThrThrCyCySeSerArgArgSerLySThrThrHisLeu	557
Db	1990	TCACAACAAGAGATCACACGACCTGCTGTTCACACACACACAAAAAACTTTTGGCATTC	2049
QY	558	ProAsnSerAnLeuProAlaThrArgLeuArgSerMetGIuGIuLeuSerThrIleHis	577
Db	2050	CCAAATGCGCAATGTATCGAAGGACCATCAAGGTATATACAAAGACTCAGACGATTCAG	2109
QY	578	IleGIuGIySerGIuGIuProSerLeuThrThrSerArgSerSerLeuAsnLeuLybAla	597
Db	2110	ATCAGATGTGTGAGAGAAACCTCTGTCTAAACGCCGATCATGTTTAAATGCCAAATG	2169
QY	598	AspAspGIyLeuLeuArgProAsnCyLySThrSerGIuIleThrThrAlaIleIleSerIle	617
Db	2170	GAAAGGTGTGTTAACTAACTGTCACAAACCTTATGTGACTTACGACGCAATATATAGATC	2229
QY	618	ProThrProProAlaLeuThrProGIuGIyGIuSerArgPro-----ProProAlaser	635
Db	2230	CCAAcACTTCAGTACACACACACAGAGACAGATAGGCCAGAAATCCCTCGATGATCTCA	2289
QY	636	ProGIyProAsnThrAsnIleProSerIleThrSerAsnValValLySValSerValLeu	655
Db	2290	GGAGGA-----AATATTGTCAcAGTTTCTGCTTTG	2319

AC ADM10922;  
XX 20-MAY-2004 (first entry)  
XX  
XX  
DE Human O647SgenomicContig3 homologue cDNA #4.  
XX  
XX  
XX ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;  
XX cytosolic; gene therapy; human; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2003206918-A1.  
XX  
XX 06-NOV-2003.  
XX  
XX 05-FEB-2003; 2003US-00361811.  
XX  
XX 10-SEP-1999; 99US-00394374.  
XX 01-MAY-2000; 2000US-00561778.  
XX 15-AUG-2000; 2000US-00640173.  
XX 07-SEP-2000; 2000US-00656668.  
XX 14-NOV-2000; 2000US-00713550.  
XX 03-APR-2001; 2001US-00825294.  
XX 02-OCT-2001; 2001US-00970966.  
XX 02-AUG-2002; 2002US-00212677.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Fanger GR, Fling SP;  
XX  
XX WPI; 2003-901037/82.  
XX P-PSDB; ADM10928.  
XX  
XX New polynucleotides encoding tumor proteins, treating or inhibiting the  
XX development of cancer, particularly ovarian cancer, and for stimulating  
XX and/or expanding T cells specific for a tumor protein.  
XX  
XX  
XX Example 12; SEQ ID NO 253; 221pp; English.  
XX  
XX This invention describes a novel ovarian tumour protein which can be used  
XX to detecting the presence of an ovarian tumour protein in a patient by  
XX stimulating and/or expanding T cells specific for the tumour protein. The  
XX products of the invention can also be used in a method to inhibit the  
XX development of a cancer in a patient comprising (a) incubating CD4+  
XX and/or CD8+ T cells isolated from a patient with at least one ovarian  
XX tumour protein, such that T cell proliferate and (b) administering to the  
XX patient the proliferated T cells. The cytosolic polynucleotides or  
XX polypeptides described in the invention are useful for treating or  
XX inhibiting the development of cancer, particularly ovarian cancer and for  
XX stimulating and/or expanding T cells specific for a tumour protein or for  
XX gene therapy.  
XX  
XX  
XX Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;  
XX  
XX  
XX Alignment Scores:  
XX Pred. No.: 6.57e-200 Length: 2351  
XX Score: 2498.50 Matches: 486  
XX Percent Similarity: 84.09% Conservative: 69  
XX Best Local Similarity: 73.64% Mismatches: 70  
XX Query Match: 73.23% Indels: 35  
XX DB: 11 Gaps: 7  
XX  
XX US-10-062-879-2 (1-655) x ADM10922 (1-2351)  
XX  
XX  
XX 1 MetAlaAlaGlyValAlaAlaATrPLeuProPheAlaArgAlaAlaAlaIleGlyTTPMet 20  
XX 430 ATGGGGGGGGGGGTGGCAAGCGTGTCTTTGCAAGGGCGAGCGGCTATCGGGTGGATG 489  
XX  
XX 21 ProValAlaAsnCyProMetProLeuAlaPcoAlaAspLysAsnLysArg--GlnAsp 39  
XX Db 430 CCTGTGGCTCGGGGGCTATGCGGCTCCCGGAGCGAAGAGAAAGAACCCCAAGAT 549  
XX 40 GiueuileValleuAsnValserGlyArgArgpHeGlnThrTTPArgThrThreLeuGlu 59







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Qy 278 AsnAsnGluAspValSerGlyValAlaPheValThrLeuArgValPheArgValPheArgTlle 297
Db 1270 GACATATGAGACGTCAGCGAGGCTTTGTCTACACTCCGAGCTTCCGGGTCTTCAGAGATC 1329
Qy 298 PheLysPheSerArgHisSerGlnGlyLeuArgTlleLeuGlyTyrThrLeuLysSerCys 317
Db 1330 TTTAAGTTTCCCGCCACTCTCAAGGCTCGGCATCTCGGGGTACACACTAGAGAGTGTGT 1389
Qy 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
Db 1390 GCCTCAGAAATGGGCTTGTGCTTTCTCGCTCAACATGATCATCATCTATCTGCTACACA 1449
Qy 338 ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerTlleProAlaSer 357
Db 1450 GTTATGTTCTTCAGAGAGAGAGGCTCTCGCTGAGCAAGTTCAACAGCATCTCCGACACC 1509
Qy 358 PheTyrPyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377
Db 1510 TTCTGTATACCATGTCATCATGACATCAACTAGGGATGGTGATGATGTCGCAAAATCC 1569
Qy 378 IleAlaGlyLysIlePheGlySerTlleCysSerLeuSerGlyValLeuValIleAlaLeu 397
Db 1570 ATAGCAGAGAGAAATTTGTGTTCTATCTGTTGCTGAGTGGGGTCTTGCTATTGCTCTTA 1629
Qy 398 ProValProValIleValSerAsnPheSerArgTlleTyrHisGlnAsnGlnArgAlaAsp 417
Db 1630 CCGTTCGGGATGTATGATCACTCACTGATCTGATCTCAACCAAGAAATCAACGAGCAGAC 1689
Qy 418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgTlleArgValAlaLysThrGlySer 437
Db 1690 AAACGAGAGGCGACAAAGAAAGCTAGACTGCGCAGATCCGGGCGACCAAAAGGAGAAC 1749
Qy 438 SerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThr 457
Db 1750 GCAATGCTTACATGACAGCAAGCAAGGATGTTTACTCACTAATCACTGCTCAG---TCC 1806
Qy 458 GlyThrProGluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477
Db 1807 TCAGAGAGATGAGCGGCTTTGTAGCAAAATCCGGCTTCACGCTTTGAAACCCACACACAC 1866
Qy 478 HisLeuLeuHisCysLeuGluLysThrThrGlyLeuSerTyrLeuValAspAspProLeu 497
Db 1867 CACCTGCTTCACTCCCTGGAAAAAACACG----- 1896
Qy 498 LeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGlu 517
Db 1897 -----AATCAGAGATTTGTGAGCAAGCAAGATCTTTGAA 1929
Qy 518 GlnAsnGlyMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSer 537
Db 1930 GAAAGCTGCATGAAAGTTGCAACTGTTAATGTCCTTCAATGCACAGTCCCTTCAGTCTCT 1989
Qy 538 SerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysLysThrThrHisLeu 557
Db 1990 TCACAAAGAGAGACACAGACCTGCTTTCACAGACACCAAAAACTTTCCGATC 2049
Qy 558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHis 577
Db 2050 CCAATGCAATGATATCAGAGAACCATCAAGGTAGTATACAAAGATCTCAGACAGATTCAG 2109
Qy 578 IleGlnIlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLysAla 597
Db 2110 ATCAGATGTGTGAGAGAAACCTCTGTCTAAGCGCATCCAGTTTAAATGCCAAATG 2169
Qy 598 AspAspGlyLeuArgProAsnGlyLeuThrSerGlnIleThrThrAlaIleIleSerTlle 617
Db 2170 GAAGAGTGTGTAAACTAAATGTGAACAACCTTATGATACAGCAATATAAGATC 2229
Qy 618 ProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAlaSer 635
Db 2230 CCAACACCTCCAGTACACACACAGAAAGAGACGATAGCGCAGATCCCTGAGTACTCA 2289

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Qy 636 ProGlyProAsnThrAsnIleProSerTlleThrSerAsnValLysValSerValLeu 655
Db 2290 GGAGGA-----AATATTGTCAGAGTTTCTGCTTGG 2319

RESULT 11
ADM10923
ID ADM10923 standard; cDNA; 5333 BP.
XX
AC ADM10923;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human O647SgenomicContig3 homologue cDNA #5.
XX
KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KW cyrostatic; gene therapy; human; ss.
XX
XX Homo sapiens.
XX
PN US2003206918-A1.
XX
PD 06-NOV-2003.
XX
PE 05-FEB-2003; 2003US-00361811.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fanger GR, Fling SP;
XX
DR WPI: 2003-901037/82.
XX
DR P-PSDB; ADM10929.
XX
PT New polynucleotides encoding tumor proteins, treating or inhibiting the
PT development of cancer, particularly ovarian cancer, and for stimulating
PT and/or expanding T cells specific for a tumor protein.
XX
XX Example 12; SEQ ID NO 254; 221bp; English.
XX
PS This invention describes a novel ovarian tumour protein which can be used
CC to detecting the presence of an ovarian cancer in a patient by
CC stimulating and/or expanding T cells specific for the tumour protein. The
CC products of the invention can also be used in a method to inhibit the
CC development of a cancer in a patient comprising (a) incubating CD4+
CC and/or CD8+ T cells isolated from a patient with at least one ovarian
CC tumour protein, such that T cell proliferate and (b) administering to the
CC patient the proliferated T cells. The cytostatic polynucleotides or
CC polypeptides described in the invention are useful for treating or
CC inhibiting the development of cancer, particularly ovarian cancer and for
CC stimulating and/or expanding T cells specific for a tumour protein or for
CC gene therapy.
XX
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,15e-199 Length: 5333
Score: 2498.50 Matches: 486
Percent Similarity: 84.09% Conservative: 69
Best Local Similarity: 73.64% Mismatches: 70
Query Match: 73.23% Indels: 35
DB: 11 Gaps: 7

US-10-062-879-2 (1-655) x ADM10923 (1-5333)
Qy 1 MetAlaIleGlyValAlaIleAlaIleThrLeuProPheAlaArgAlaIleAlaIleGlyTyrPMet 20

```

Db 966 ATGGCGGCGGGGTGGCAGCTGGCTGCTTTTGGCAAGGCGACGGCTATCGGGTGGATG 1025  
 Qy 21 ProValAlaIasnCySPrometProLeuAlaProAlaAspIysAsnIysArg---GlnAsp 39  
 Db 1026 CCGTGGGCTCGGGGCGCTATGCGGCTCCCGGAGGCGAGAGAGAAAGAACCCAAAGAT 1085  
 Qy 40 GluLeuIleValLeuAsnValSerGIYArgArgPheGlnThrTrpArgThrIleuGlu 59  
 Db 1086 GCTCTCATTTGTGCTGAATGTGAATGTGACCCGCTTCACAGCTGGAGAGACACCCCTGGAA 1145  
 Qy 60 ArgTYrProAspThrIleuLeuGIYSerThrGluIysGluPhePheAsnGluAspThr 79  
 Db 1146 CGTTACCCACACACTCTACTGGGCACTTCTGAGAGGGACTTTTCTTACCAACCCAGAAACT 1205  
 Qy 80 LysGIuTYrPhePheAspArgAspProGIuValPheArgCyValLeuAsnPheTYrArg 99  
 Db 1206 CAGAGATATTTCTTTGACCTGACCCAGACATCTCCGCAACCTCGAATTTCTACCCG 1265  
 Qy 100 ThrGIYIysLeuIleSTYrProArgTYrGIuCyAlIeSerAlaTYrAspAspGIuLeuAla 119  
 Db 1266 ACTGGAGAGCTCCACTATCTCGCCACAGATGCATCTGCTTACATGAAGAACTGGCC 1325  
 Qy 120 PheTYrGIYIleLeuProGIuIleIleGIYAspCySerTYrGIuGIuTYrIysAspArg 139  
 Db 1326 TTCTTGGCTCATCCCGGAAATCATGCGGCACTGCTTTATGAGAGTACAAAGATCCG 1385  
 Qy 140 LysArgGIuAsnAlaGIuArgIeMetAspAspAsnAspSerGIuAsnAsnGIuIysSer 159  
 Db 1386 AGCGAGAGAGAACCCCGGCGCTGACAGACGACGGGATACGACACCGCTGGGAGAGAC 1445  
 Qy 160 ---MetProSerIeuserPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThr 178  
 Db 1446 GCCTTGCCCACTGATCGAAGGCGAGAGGGTCTGAGGGCTTCGAGAAACCCCAACCC 1505  
 Qy 179 SerThrLeuAlaLeuValPheTYrTYrValThrGIYpHePheIleAlaValSerValIle 198  
 Db 1506 AGCAGATGGCCCTGGGTGTTCTACTATGTACACGGGGTTTTCATGCGCTCTGTGCATC 1565  
 Qy 199 ThrAsnValValGIuThrValProCYGIYThrValProGIYSer---LysGIuLeuPro 217  
 Db 1566 GCGAATGTGGTGAAGAACAGTGGCGGTGATCAAGCCAGGTCACTTAAAGAACTGGCC 1625  
 Qy 218 CySGIYGIuArgTYrSerValAlaPhePheCyLeuAspThrAlaCyValMetIlePhe 237  
 Db 1626 TGTGGAGAGCGGATGTGTGGGCTTCTCTGCTTGACAGCGCTGCCGATGATCTTC 1685  
 Qy 238 ThrValGIuTYrLeuLeuArgLeuPheAlaAlaProSerArgTYrArgPheIleArgSer 257  
 Db 1686 ACGATTGAGATTGCTTCCGCTGGCTGACGCGCTTATGCTTACCGTTTGTGCTAGT 1745  
 Qy 258 ValMetSerIleIleAspValValAlaIleMetProTYrTYrIleGIYLeuValMetThr 277  
 Db 1746 GTATGATGATTCATCGACGTGTGGCCATCTGCTTATTAATGGGCTGGATGACA 1805  
 Qy 278 AsnAsnGIuAspValSerGIYAlaPheValThrLeuArgValPheArgValIle 297  
 Db 1806 GACAAATAGGACGTCAACGAGGCTTGTGTCACTCGAATCTTCCGGGCTTCAGAGATC 1865  
 Qy 298 PheLysPheSerArgHisSerGIYNGIYLeuArgIleuGIYTYrThrIleuLysSerCyS 317  
 Db 1866 TTTAAGTTTCCGCCACTCTCAAGGCTGGGATCTGGGATGACACTGAAGAGTGT 1925  
 Qy 318 AlIserGIuLeuGIYpHeLeuLeuPheSerIleuThrMetAlaIleIleIlePheAlaThr 337  
 Db 1926 GCGTCAAAATTTGGGCTTCTTGCTTTCTCGCTACCACTGCTATCATCATCTTCGCTACA 1985  
 Qy 338 ValMetPheTYrAlaGIuLysGIYSerSerAlaSerIysPheThrSerIleProAlaSer 357  
 Db 1986 GTTATGTCTTACGAGAGAGGGGTCTTCCGCTTAGCAAGTTCAACGACATCCCTGAGAGC 2045  
 Qy 358 PheTrpTYrThrIleValThrMetThrThrLeuGIYTYrGIYAspMetValProLysThr 377

Db 2046 TTCTGTATACCATGTCACCATGACAAACCTAGGGTATGTTGATCATGTGCCAAAAACC 2105  
 Qy 378 IleAlaGIYIysIlePheGIYSerIleCySerIeuserGIYValLeuValIleAlaLeu 397  
 Db 2106 ATAGCAGGAGAGATTTTGTGTTCTATCTGTTCGTGATGGGGCTTGGTCACTTGTCTA 2165  
 Qy 398 ProValProValIleValIserAsnPheSerArgIleTYrHisGlnAsnGIYAspAlaAsp 417  
 Db 2166 CCGTTCGGGTGATGTATCCAACTTCAGTCAGTCATCTTACACAGAAATCAACAGACAGAC 2225  
 Qy 418 LysArgArgAlaGlnIysLysAlaArgLeuAlaArgIleArgValAlaIysThrGIYSer 437  
 Db 2226 AAACGAGAGGACAAAGAAAGCTGACCTGGCCAGATCCGGGCGCAAGGCGAAAGCGAAGC 2285  
 Qy 438 SerAsnAlaTYrLeuHisSerIysArgAsnGIYLeuLeuAsnGIuAlaGIuLeuThr 457  
 Db 2286 GCAAAATGCTTACATGACGAGCAAGCAAGAAATGTTTACTCAGTATTCAGCTGGCAG---TCC 2342  
 Qy 458 GIYThrProGIuGIuGIuHisMetGIYIysThrThrSerLeuIleGIuserGlnHis 477  
 Db 2343 TCAGAGATGAGCAGGCTTTGTTTACGAAATCCGGCTTCAGCTTGGAAACCCAGACACAC 2402  
 Qy 478 HisLeuLeuHisCySLeuGIuLysThrThrGIYLeuSerTYrLeuValAspAspProLeu 497  
 Db 2403 CACCTGTTCACTGCTGGAAAAAACACG----- 2432  
 Qy 498 LeuSerValArgThrSerThrIleLysAsnHisGIuPheIleAspGIuGlnMetPheGlu 517  
 Db 2433 -----AATCAACAGTTTGTGGACGAAACAAGCTTTTGAA 2465  
 Qy 518 GlnAsnCyMetGIuserSerMetGlnAsnTYrProSerThrArgSerProSerLeuSer 537  
 Db 2466 GAACCTCATGAGAAAGTTGCACTGTATATGTCTTCAAGTCAAGTCTTCACTCTCT 2525  
 Qy 538 SerHisProGIYLeuThrThrCYeCySerArgArgSerIysLysThrThrHisLeu 557  
 Db 2526 TCACAAACAAGAGTCAACAGACCTGCTTCAAGACACAAAAAACTTTCGCATC 2585  
 Qy 558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnIuLeuSerThrIleHis 577  
 Db 2586 CCAATGTCCAATGTATCAGAGAACCAATCAAGTGTATACAAAGAACTCAGACCATTCAG 2645  
 Qy 578 IleGlnGIYSerGIuGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAla 597  
 Db 2646 ATCAGATGTGTGAGAGAAACCTCTGTCTTAAACGCGCATCACTTTAAATGCCAAATG 2705  
 Qy 598 AspAspGIYLeuArgProAsnCySLeuThrSerGlnIleThrThrAlaIleIleSerIle 617  
 Db 2706 GAAGAGTGTGTTAACTTAACTGTAACAACCTTATGACTACAGCAATATATAGCATC 2765  
 Qy 618 ProThrProProAlaLeuThrProGIuGIYGIuserArgPro-----ProProAlaSer 635  
 Db 2766 CCAACACCTCCAGTAAACACACAGAAAGAAACCATATGGCCAGATCCCTGAGTACTCA 2825  
 Qy 636 ProGIYProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerValLeu 655  
 Db 2826 GGAGGA-----AATATTGTCAAGAGTTTGTGCTTTG 2855  
 RESULT 12  
 ID ADM10921  
 AC ADM10921 standard, cDNA, 5333 BP.  
 AC ADM10921;  
 DT 20-MAY-2004 (first entry)  
 DE Human O6478genomicContig3 homologue cDNA #3.  
 KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;  
 KW cytosolic; gene therapy; human; ss.  
 OS Homo sapiens.



PN US2003206918-A1.  
 XX  
 PD 06-NOV-2003.  
 XX  
 PF 05-FEB-2003; 2003US-00361811.  
 XX  
 PR 10-SEP-1999; 99US-00394374.  
 PR 01-MAY-2000; 2000US-00561778.  
 PR 15-AUG-2000; 2000US-00640173.  
 PR 07-SEP-2000; 2000US-00556668.  
 PR 14-NOV-2000; 2000US-00713550.  
 PR 03-APR-2001; 2001US-00825294.  
 PR 02-OCT-2001; 2001US-00970966.  
 PR 02-AUG-2002; 2002US-00212677.  
 XX  
 PA (CORI-) CORIYA CORP.  
 PI Fanger GR, Fling SP;  
 XX WPI: 2003-901037/82.  
 DR P-PSDB: ADM10927.  
 XX  
 PT New polynucleotides encoding tumor proteins, treating or inhibiting the  
 PT development of cancer, particularly ovarian cancer, and for stimulating  
 PT and/or expanding T cells specific for a tumor protein.  
 XX  
 PS Example 12; SEQ ID NO 252; 221bp; English.  
 XX  
 CC This invention describes a novel ovarian tumour protein which can be used  
 CC to detecting the presence of an ovarian cancer in a patient by  
 CC stimulating and/or expanding T cells specific for the tumour protein. The  
 CC products of the invention can also be used in a method to inhibit the  
 CC development of a cancer in a patient comprising (a) incubating CD4+  
 CC and/or CD8+ T cells isolated from a patient with at least one ovarian  
 CC tumour protein, such that T cell proliferate and (b) administering to the  
 CC patient the proliferated T cells. The cytostatic polynucleotides or  
 CC polypeptides described in the invention are useful for treating or  
 CC inhibiting the development of cancer, particularly ovarian cancer and for  
 CC stimulating and/or expanding T cells specific for a tumour protein or for  
 CC gene therapy.  
 XX  
 SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 2,15e-199 Length: 5333  
 Score: 2498.50 Matches: 486  
 Percent Similarity: 84.09% Conservative: 69  
 Best Local Similarity: 73.64% Mismatches: 70  
 Query Match: 73.23% Indels: 35  
 DB: 11 Gaps: 7  
 US-10-062-879-2 (1-655) x ADM10921 (1-5333)  
 QY 1 MetAlaIaGlyValAlaAlaTPrLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet 20  
 Db 966 ATGGCGGCGGGGGGCGGCGAGCTGGCTGCTTTTCAGAGGCGAGCGGCTATGGGTGATG 1025  
 QY 21 ProValAlaAsnCySPrometProLeuAlaProAlaAspLyAsnLySArg--GlnAsp 39  
 Db 1026 CTTGTGCTCTCGGGGCTATGCTCCCGGAGGCGAGAGAGGAAAGAACCCAGAT 1085  
 QY 40 GlnLeuIleValIleuAsnValSerGlyAArgAArgPheGlnTrpAArgThrThleuGlu 59  
 Db 1086 GCTTCATGTGCTGAATGTAGTGGCACCGCTTCCAGACGTGGCAGACACCCCTGGAA 1145  
 QY 60 ArgTyrProAspThrIleuLeuGlySerThrGluysGluPhePheAsnGluAspThr 79  
 Db 1146 CGTTACCAAGACACTCTACTGGCAGTTCTGAGAGGACTTTTCTACCAACCAAGAACT 1205  
 QY 80 LysGluTyrPhePheAspAArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99  
 Db 1206 CAGCAGTATTTCTTTGACCGGTGACCCAGACATCTTCCGCCACATCCGTAATTTCTACCGC 1265

QY 100 ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119  
 Db 1266 ACTGGAAAGCTCCACTATCTCGCGACAGTGCATCTCTGCTTACGATGAAGAACTGGCC 1325  
 QY 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGlyGluTyrLysAspArg 139  
 Db 1326 TTTCTTGGCTTCATCCCGGAATCATCGGCACATGCTGTATTGAGAGTAAAGATGCG 1385  
 QY 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnGlnGluSer 159  
 Db 1386 AGGCGAGAGAAAGCGCGAGCGCTTCAGAGACACCGGATACCGACACCGCTGGGAGAGC 1445  
 QY 160 --MetProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThr 178  
 Db 1446 GCCTTGCCACCAACATGCTGCAAGGCAAGAGGCTCTGAGAGGCTTCGAGAACCCCAACCC 1505  
 QY 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198  
 Db 1506 AGCAGATGGCCCTGAGTGTCTACTATGTCACGGGGTATTTTCATTGCGCTCTGTCAATC 1565  
 QY 199 ThrAsnValAlaGluThrValProCysGlyThrValProGlySer--LysGluLeuPro 217  
 Db 1566 GCGAATGTGTGGAACAGAGCGCTGCGGATCAAGCCAGTCACTTAAGAACTGCC 1625  
 QY 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db 1626 TGTGAGAGCGGATATGCTGTGGCTTCTTCTGCTTGAACAGGCTCGCTCATATCTTC 1685  
 QY 238 ThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257  
 Db 1686 ACAGTTAGATTTGCTTGGCTGGCTGGAGCGCTGATGCTGATCCCTTTGTGCTGATGT 1745  
 QY 258 ValMetSerIleIleAspValAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
 Db 1746 GTCATGAGTATCATCGACGAGTGGTCCATCTGCTTATTCATATGGAGCTGTGATGACA 1805  
 QY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297  
 Db 1806 GACATATGACATGCTCAGCGAGCTTGTCTACATCCGAGCTTCCGGGTCTTACAGATC 1865  
 QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317  
 Db 1866 TTTAAGTTTCCCGCACCTCTCAAGGCTCGGCGATCTCGGGGTACACATGAAGATTGT 1925  
 QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr 337  
 Db 1926 GCCTCAGAAATTTGGCTTCTTGTCTTCTGCTCAACATGGCTATCATCATCTTGGTACA 1985  
 QY 338 ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357  
 Db 1986 GTTATGTCTTACGAGAGAGGGGTCTTCGGCTAGCAAGTTTACCAAGATCCCTGCAAGC 2045  
 QY 358 PheTyrTyrThrIleValIleThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377  
 Db 2046 TTCGTATACATCGTACATGACATGACAACTAGGATAGTGTACATGGTCCAAAAACC 2105  
 QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
 Db 2106 ATACAGAGGAAGATTTTGTGCTTATCTGTTCGTGAGTGGGTCTTGGCATATGCTCTA 2165  
 QY 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417  
 Db 2166 CTTGTCCGGTATGTATTCACACTTATGATGCGATCTTACCAACCAAGATCCAGCGAGAC 2225  
 QY 418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysSerGlySer 437  
 Db 2226 AAAAGAGGGGACAAAGAAAGCTAGACTGCGCAGATCCGGGACGCAAAAGGGAAGC 2285  
 QY 438 SerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
 Db 2286 GCAATCTTATCATGACAGCAAGAAAGGATTTACTAGTATCAAGCTGACG--TCC 2342  
 QY 458 G1TyrProGluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477



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Db      2343 TCAGAGATAGAGAGGCTTTGTTAGCAAAATCCGGCTTCCAGCTTTAAACCCAGACACAC 2402
Qy      478 HileuleuHisiCysLeuGluGluYThrThrGlyLeuSerYrLeuValAspAspProLeu 497
Db      2403 CACCTGCTTACCTGCTCCGAAAAAACACAC----- 2432
Qy      498 LeuSerValArgThrSerThrIleYsAsnHisiGluPheIleAspGluGluMetPheGlu 517
Db      2433 -----AATCAGAGTGTGTGACCAACAGACCTTTGAA 2465
Qy      518 GluAsnCysMetGluSerSerMetGluAsnYrProSerThrArgSerProSerLeuSer 537
Db      2466 GAAGGCTGATGAGAGTGAACCTGTTAATCGTCTTCAAGTCACAGTCTTCACTGCT 2525
Qy      538 SerHisProGlyLeuThrThrThrCysCysSerArgSerSerYsLeuThrHisLeu 557
Db      2526 TCACACAGAGAGTACACACACCTGCTGTTCAAGACACACAAAAAATTTCGCATC 2585
Qy      558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGluGluLeuSerThrIleHis 577
Db      2586 CCAATGCTCAATGATATCAGAGACCATCAAGTAGATATACAAAGACTCAGCAGATTGAG 2645
Qy      578 ILGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuVal 597
Db      2646 ATCAGATGTGTGAGAGACACCTCTGTCTTAACAGCCGATCCAGTTAAATGCCAAATG 2705
Qy      598 AspAspGlyLeuArgProAsnCysLysThrSerGlnLeuThrAlaIleLeuSerIle 617
Db      2706 GAAGAGTGTGTAACTAACTGAACACACTTATGTGACTACAGCAATATATATACATC 2765
Qy      618 ProThrProAlaLeuThrProGlyGlyLeuSerArgPro-----ProProAlaSer 635
Db      2766 CCAACACCTCCAGTAAACCAACCAAGAGAGACATATGAGCCCAATATCCCTGAGTACTCA 2825
Qy      636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValIleValSerValLeu 655
Db      2826 GAGAGA-----AATATGTCTCAGAGTTCTGCTTGG 2855

RESULT 13
ADJ11253
ID ADJ11253 standard; DNA; 5333 BP.
XX
AC ADJ11253;
XX
DT 15-APR-2004 (first entry)
XX
DE Human ovarian tumour antigen DNA SegID 254.
XX
KW human; dg; ovarian cancer; immunogenic; antibody;
KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
KW cyostatic; gene.
XX
OS Homo sapiens.
XX
PN US2003232056-A1.
XX
PD 18-DEC-2003.
XX
PF 14-FEB-2003; 2003US-00369186.
XX
PR 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
PR 02-AUG-2002; 2002US-00212677.
PR 05-FEB-2003; 2003US-00361811.
XX
PA (CORI-) CORIYA CORP.
XX

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PI Fanger GR, Fling SP;
XX
XX WPI; 2004-178717/17.
DR P-PsDB; ADJ11259.
XX
XX Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT polypeptide, useful as probes of primers for detecting presence of cancer
PT in a patient.
XX
XX Example 12; SEQ ID NO 254; 222pp; English.
XX
XX This invention relates to novel isolated polynucleotides and methods for
CC the therapy and diagnosis of cancer, particularly ovarian cancer.
CC Specifically, it refers to these polynucleotides and the encoded
CC polypeptides thereof, as well as immunogenic peptides, antibodies,
CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC that are targeted to those cells expressing the proteins of interest. The
CC present invention describes methods that are useful for stimulating and/
CC or expanding T cells specific for a tumourigenic protein (i.e. T cell
CC therapy). Furthermore, compositions can be used for the diagnosis,
CC treatment and/ or prevention of ovarian cancer by stimulating an immune
CC response in a patient. Accordingly, these compositions exhibit cytostatic
CC activity. This polynucleotide is a human ovarian tumour antigen DNA
CC sequence given in an exemplification of the invention.
XX
XX SEQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other:

Alignment Scores:
Pred. No.: 2,15e-199 Length: 5333
Score: 2498.50 Matches: 486
Percent Similarity: 84.09% Conservative: 69
Best Local Similarity: 73.64% Mismatches: 70
Query Match: 73.23% Indels: 35
DB: Gaps: 7

US-10-062-879-2 (1-655) x ADJ11253 (1-5333)
Qy 1 MetAlaAlaGlyValAlaAlaTTrpLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet 20
Db 966 ATGGCGGCGGGGCGGCGGCGCTGCTGCTTTTCAAGGCGAGCGGCTATCGGGTGATG 1025
Qy 21 ProValAlaAsnCySPrometProLeuAlaProAlaAspLysAsnYsArg---GluAsp 39
Db 1026 CCGTGGGCTCGGGGCGCTATCGCGCTCCCGAGGAGGAGAGCAAAAGAACCCAGAT 1085
Qy 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59
Db 1086 GCTCTCATGTGCTGAATGATGATGAGTGCACCGCTTCCAGACGTGCGAGACACCTTGAA 1145
Qy 60 ArgYrProAspThrLeuLeuGlySerThrGluYsGluPhePheAsnGluAspThr 79
Db 1146 CGTTACCCAGACACTCTACTGGGCGATTCAGAGGAGCATTTTCTACCAACCCAGAAACT 1205
Qy 80 LysGluYrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheYrArg 99
Db 1206 CAGCAGTATTTCTTGGACCGGATCCGACCAACATCTTCGCAATCTGAATTTCTACCGC 1265
Qy 100 ThrGlyLysLeuHisiYrProArgYrGluCysIleSerAlaYrAspAspGluLeuAla 119
Db 1266 ACTGGAAGCTCCACTATCTCTGCGACAGAGTCACTCTGTTACGATGAAGAACTGGCC 1325
Qy 120 PheYrGlyIleLeuProGluIleIleGlyAspCysYrGluGluYrYrLysAspArg 139
Db 1326 TTCTTGGCTCATCCCGGAATATCATCGGACATGCTGTATGAGAGTCAAGATCGC 1385
Qy 140 LysArgGluAsnAlaGluArgLeuMetCAspAspAsnAspSerGluAsnAsnGluGluSer 159
Db 1386 AGCGCAGAGAAACCGCGAGCGCTCGACAGACCAACCGGATACCGACACCGCTGGGAGAGC 1445
Qy 160 ---MetProSerLeuSerPheArgGluThrMetTrpArgAlaPheGluAsnProHisThr 178
Db 1446 GCCTTGCCACCATGACTGCAGAGGAGGAGGTCTGAGAGGCTTCGAGAACCCCAACACC 1505

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Qy 179 SerThrLeuAlaLeuValPheTYrTYrValThrGlyPhePheIleAlaValSerValIle 198
Db 1506 AGACAGCATGGCCCGGTGTTTACTATGATGTCACGGGGTTTTTCATTCGGCTCTGTCATC 1565
Qy 199 ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
Db 1566 GCGCATGTGGTGGAAACAGTCCCTGGCGATCAAGCCAGCTCATTAAGAACTGCGCC 1625
Qy 218 CysGlyGluArgTYrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db 1626 TGTGGAGAGCGGATGGCTGTGGCTTCTGTCTGTGGACAGCGCTGGCTGTATATCTTC 1665
Qy 238 ThrValGluTYrLeuLeuArgLeuPheAlaAlaProSerArgTYrArgPheIleArgSer 257
Db 1686 ACGATTGAGATTGTTGCTTCGCTGGCTGCAGCGCTGTGTTACCGTTTGTGCGTAGT 1745
Qy 258 ValMetSerIleIleAspValValAlaIleMetProTYrTYrIleGlyLeuValMetThr 277
Db 1746 GTCATGAGTATCATCGACGTGTGGCCATCCGCTTATTCATTGGGGCTGGTATGACA 1805
Qy 278 AsnAsnGluAspValSerGlyValaPheValThrLeuArgValPheArgValPheArgIle 297
Db 1806 GACAAATGAGACGTCAGCGGAGCTTGTACACTCCGAGCTTCCGGCTTTCAGGATC 1865
Qy 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTYrThrLeuLysSerCys 317
Db 1866 TTTTAACTTTCCCGCCACTCTCAAGGCTCGCATCTCGGGGTACACACTGAAAGTTGT 1925
Qy 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr 337
Db 1926 GCCTCAAAATGGGCTTCTTGCTTTCTCGCTCAACATGGCTATCATCATCTTGCTACA 1985
Qy 338 ValMetPheTYrAlaGlyGlySerSerAlaSerIlePheThrSerIleProAlaSer 357
Db 1986 GTATATGTTCTACACAGAAAGGGGTCTTCGCTTACGAAAGTTTACACACATCCCTCGAGCC 2045
Qy 358 PheTYrTYrThrIleValThrMetThrThrLeuGlyTYrGlyAspMetValProLysThr 377
Db 2046 TTTCTGATATCCATCGTACCATACACACTAAGGATGTGTGCATGTGTCCAAAAACC 2105
Qy 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397
Db 2106 ATAGCAGGGAAGATTTTGGTTCATCTGTTCCGTGAGGGGCTTGGTTCATTGCTCTA 2165
Qy 398 ProValProValIleValSerAsnPheSerArgIleTYrHisGlnAsnGlnArgAlaAsp 417
Db 2166 CCGTTCCTCGGTGATTTGATTCAACTTCACTGATCTTCAACCAAGATCAACGAGCAGAC 2225
Qy 418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437
Db 2226 AAACGAAAGGCGACAAAGAAAGCTAGACTGGCCAGATCCGGGCGACCAAAAGCGGAAGC 2285
Qy 438 SerAsnAlaTYrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457
Db 2286 GCAAAATGCTTACATGACAGCAAAACGAAATGTTTACTCATGATACAGCTGACAG---TCC 2342
Qy 458 GlyThrProGluGluGlnHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477
Db 2343 TCAGAGGATAGCAGCGCTTTTGTAGCAAAATCCGCGCTTCAAGCTTTGAAACCCACACAC 2402
Qy 478 HisLeuLeuHisCysLeuGlnLysThrThrGlyLeuSerTYrLeuValaAspProLeu 497
Db 2403 CACCTGCTTACAGCTGCTGAAAAAACACAG--- 2432
Qy 498 LeuSerValaArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGlu 517
Db 2433 -----AATCAGCAAGTTTGGAGCAAGCAAGCTTTTGA 2465
Qy 518 GlnAsnCysMetGluSerSerMetGlnAsnTYrProSerThrArgSerProSerLeuSer 537
Db 2466 GAAAGCTGATGAAAGTTTGAACATGTTATTCGTTCAAGTTCACAGTCTTCACTGTCT 2525
Qy 538 SerHisProGlyLeuThrThrThrCysCysSerArgLysSerLysLysThrThrHisLeu 557

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Db 2526 TCACAAACAGAGACACACACACCTGCTTCAAGACACAAACAACTTTTGGCATC 2585
Qy 558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluSerThrIleHis 577
Db 2586 CCAAAATCCATGATATCAGAGAGACCATCAAGTATTAACAGAACTCAGCAGATTTCAG 2645
Qy 578 IleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLysAla 597
Db 2646 ATCAGATGTGTGAGAGAAACACCTCTGTCTAACAGCCGATCCAGTTTAAATCCAAATG 2705
Qy 598 AspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleIleSerIle 617
Db 2706 GAAAGTGTGTAAACTTAACTGTAACCACTTATGTGACTACAGCAATATATAGCATC 2765
Qy 618 ProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAlaSer 635
Db 2766 CCAACACCTCAGTAAACACACAGAGAGACATGGCCAGAAATCCCTGAGTACTCA 2825
Qy 636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerValLeu 655
Db 2826 GAGAGA-----AATATTGTCAAGATTCTGCTTTC 2855

RESULT 14
ADJ11251
ID ADJ11251 standard; DNA; 5333 BP.
AC
XX ADJ11251;
XX
XX 15-APR-2004 (first entry)
XX
DE Human ovarian tumour antigen DNA SeqID 252.
XX
XX human; ds; ovarian cancer; immunogenic; antibody;
XX antigen presenting cell; APC; immune system cell; T cell; tumorigenic;
XX cytosolic; gene.
XX
XX Homo sapiens.
XX
XX US2003232056-A1.
XX
XX 18-DEC-2003.
XX
XX 14-FEB-2003; 2003US-00369186.
XX
XX 10-SEP-1999; 99US-00394374.
XX
XX 01-MAY-2000; 2000US-00561778.
XX
XX 15-AUG-2000; 2000US-00640173.
XX
XX 07-SEP-2000; 2000US-00656668.
XX
XX 14-NOV-2000; 2000US-00713550.
XX
XX 03-APR-2001; 2001US-00825294.
XX
XX 02-OCT-2001; 2001US-00970966.
XX
XX 02-AUG-2002; 2002US-00212677.
XX
XX 05-FEB-2003; 2003US-00361811.
XX
XX (CORI-) CORIXA CORP.
XX
XX Fanger GR, Fling SP;
XX
XX WPI; 2004-178717/17.
XX
XX P-PSDB; ADJ11257.
XX
XX Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
XX polypeptide, useful as probes of primers for detecting presence of cancer
XX in a patient.
XX
XX Example 12; SEQ ID NO 252; 222pp; English.
XX
XX This invention relates to novel isolated polynucleotides and methods for
XX the therapy and diagnosis of cancer, particularly ovarian cancer.
XX Specifically, it refers to these polynucleotides and the encoded
XX polypeptides thereof, as well as immunogenic peptides, antibodies,
XX antigen presenting cells (APCs) and immune system cells (e.g. T cells)

```

CC that are targeted to those cells expressing the proteins of interest. The  
 CC present invention describes methods that are useful for stimulating and/  
 CC or expanding T cells specific for a tumorigenic protein (i.e., T cell  
 CC therapy). Furthermore, compositions can be used for the diagnosis,  
 CC treatment and/or prevention of ovarian cancer by stimulating an immune  
 CC response in a patient. Accordingly, these compositions exhibit cytostatic  
 CC activity. This polynucleotide is a human ovarian tumour antigen DNA  
 CC sequence given in an exemplification of the invention.

XX Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	2.15e-199	Length:	5333
Score:	2498.50	Matches:	486
Percent Similarity:	84.09%	Conservative:	69
Best Local Similarity:	73.64%	Mismatches:	70
Query Match:	73.23%	Indels:	35
DB:	12	Gaps:	7

US-10-062-879-2 (1-655) x ADU11251 (1-5333)

QY 1 MetAlaIaGlyValAlaAlaIaTProPheAlaArgAlaAlaIaIaIaGlyTProMet 20  
 Db ATGGCGCGGGGGGGGCGAGCGTGGCTGCTTGGCAAGGCGACCGGTATCGGGTGGATG 1025  
 QY 21 ProValAlaAsnCySPowMetProLeuAlaProAlaAspLysAsnLysArg--GlnAsp 39  
 Db CCTGTGGCGCTCGGGGCGCTATAGCGGGCTCCCGAGGCGAGGAGGAAAGACCCAAAGAT 1085  
 QY 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59  
 Db GCTTCATATGCTGGAATGAGTGAAGTGCACCGGCTTCACAGCGTGGCGAGCACCCGGA 1145  
 QY 60 ArgTyrProAspThrLeuLeuGlySerThrGluLysGluPhePhePheAsnGluAspThr 79  
 Db CGTTACCCAGACACTCTACTGCGGCACTTCGAGAGGAGACTTTTCTTACACCCAGAAACT 1205  
 QY 80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99  
 Db CAGCAGATATTTCTTTGACCGCGACCCAGACATCTTCGCGCAATCTGGAATTTCTACCGG 1265  
 QY 100 ThrGlyLysLeuHisTyrTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119  
 Db ACTGGAGAGCTCCACTATCTCGCCACAGAGTGCATCTCTTACGATGAGAAGAACTGGCC 1325  
 QY 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArg 139  
 Db TTCTTTGGCTTCATCCCGGAATCATCGCGACTGCTGTTATGAGAGTACAGATCCG 1385  
 QY 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGlnSer 159  
 Db AGCGAGAGAAACGCCGAGCGCTGCAGAGACGACGCGATACCGACCGCTGGGGAGAGC 1445  
 QY 160 ---MetProSerLeuSerPheAspArgGlnThrMetTrpArgAlaPheGluAsnProHisTyr 178  
 Db GCCCTTGGCCCAACCACTGCGACAGGAGGAGTCTGAGGGCCCTTCGAGAAACCCCAACCC 1505  
 QY 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198  
 Db AGCAGCATGGCCCTGGTGTCTTACTATGTCAACGGGGTTTTCATTGGCCGCTCTGTCAATC 1565  
 QY 199 ThrAsnValValGluThrValProCysGlyTyrValProGlySer---LysGluLeuPro 217  
 Db GCGAATGTGTGAGAAACAGTGCCTGCGGATCAAGCCAGGTCAATTAAAGAACTGCC 1625  
 QY 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db TGTGAGAGCGGATGTGTGGCTTCTTCTGTGTGACACGGCTGCGCATGATCTTC 1685  
 QY 238 ThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257  
 Db ACAATTGATGATTTTGGCTTCCGCTGGCTGACGCGCTTACGCTTATCGTTTGTGCGTACT 1745

QY 258 ValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
 Db GTCATGAGTATCATTCAGCGTGGTCCATCTGCTTATTAATGTGGCGTGGAGTACA 1805  
 QY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297  
 Db GACATATGAGACGTTCACCGAGCTTTGTCACTCCGAGTCTTCGGGCTTCAAGATC 1865  
 QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317  
 Db TTTAAGTTTCCCGCCACTCTCAAGGCGTGGCATCTCGGGGTACACACTGAAGAGTTGT 1925  
 QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
 Db GCTTCAGATTTGGCTTCTTGGCTTTCTGCTCAACAGCTATCATCATCTTCGTCTACA 1985  
 QY 338 ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357  
 Db GTTATGTTCTACGAGAGAGGGGTCTTCGGCTAGCAAGTTTACACGATCCCTGACGCC 2045  
 QY 358 PheTyrTyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377  
 Db TTCTGTATATCATCTGCATGACATGACAACTAGGGTATGTGATCATGTGCGCAAAACC 2105  
 QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
 Db ATAGCAGGAGAAATTTTGTGTTCTATCTGTTCGTGAGTGGGGCTTGTGATATGGCTTA 2165  
 QY 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417  
 Db CCTGTTCGGTGAATTTGATCACTTCACTGATCGATCTACACAGATCAACAGAGCAGAC 2225  
 QY 418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437  
 Db AAACGAGGCGCAAAAGAAAGTACAGCTGGCCAGATCCGGGCGACCAAAAGCGGAGC 2285  
 QY 438 SerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
 Db GCAATGTCTTACGACAGAGAAACGAAATGTTTACTCGATACTGACGTGCAG--TCC 2342  
 QY 458 GlyThrProGluGluGluHisMetGlyLeuThrThrSerLeuIleGluSerGlnHis 477  
 Db TCAAGAGATGAGCAGCGCTTTGTTAGCAATCCGGCTTCAGCTTGAACCCAGACAC 2402  
 QY 478 HisLeuLeuHisCysLeuGluLysThrThrGlyLeuSerTyrLeuValAspAspProLeu 497  
 Db CACGCTTCACTGCTCGTGAATAAACACG----- 2432  
 QY 498 LeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGlu 517  
 Db -----AATCAGAGTTTGTGGACGAGCAAAAGTCTTTGAA 2465  
 QY 518 GlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSer 537  
 Db GAAAGCTGATGAGAGTTCACACTGTATATGTCTTCAAGTCAAGTCTTCACTGTCT 2525  
 QY 538 SerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysLysThrThrHisLeu 557  
 Db TACAAACAAGAGTACACAGACCTGCTTCAAGACACAAAAAAAATTTTCCGATC 2585  
 QY 558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHis 577  
 Db CCAATTTGCCAATGTATTCAGGAAGCATCAAGTGTATACAAAGAACTCAGACCAATTGAG 2645  
 QY 578 IleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLysAla 597  
 Db ATCAGATGTGTGAGAGAAACCTGTGTCTTACAGCCGATCAATTTAAATGCCAAATG 2705  
 QY 598 AspAspGlyLeuArgProAsnCysLysThrThrSerGlnIleThrThrAlaIleIleSerIle 617  
 Db GAAAGGTGTGTTAAACTAACTGAGAACAACTTATGATGACTACAGCAATATTAAGATC 2765  
 QY 618 ProThrProProAlaLeuThrProGluGluLysSerArgPro-----ProProAlaSer 635

D6									
Oy	2766 CCNAACCTCCAGTAAACAACACGAGAAGCGATAGGCCAAGATCCCTGAAGTACTCA	2825							
D6	636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValIalysValSerValLeu	655							
D6	2826 GGAGGA-----AAATTGTCAAGATTTCGCTTTG	2855							
RESULT 15									
ID	ADM43512								
AD	ADM43512 standard; DNA; 5333 BP.								
AC	ADM43512;								
XX									
DT	03-JUN-2004 (first entry)								
XX									
DE	Human ovarian cancer cDNA homologous DNA #6.								
XX									
KM	ds; human; cancer; ovarian cancer; ovarian carcinoma; gene.								
XX									
OS	Homo sapiens.								
PX	US2003129192-A1.								
XX									
PD	10-JUL-2003.								
XX									
PF	02-AUG-2002; 2002US-00212677.								
XX									
PR	10-SEP-1989; 98US-00394374.								
PR	01-MAY-2000; 2000US-00561778.								
PR	15-AUG-2000; 2000US-00640173.								
PR	07-SEP-2000; 2000US-00656668.								
PR	14-NOV-2000; 2000US-00713550.								
PR	03-APR-2001; 2001US-0085294.								
PR	02-OCT-2001; 2001US-00970966.								
XX									
PA	(CORI-) CORIXA CORP.								
XX									
PI	Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;								
XX									
DR	WPI; 2004-051070/05.								
DR	P-P8DB; ADM43518.								
PT	New isolated polynucleotide encoding an ovarian tumor protein for use in								
XX	diagnosing, preventing or treating cancer, particularly ovarian cancer.								
PS	Claim 1; SEQ ID NO 252; 220bp; English.								
CC	The invention relates to an isolated polynucleotide. The invention is								
CC	used to diagnose, prevent or treat cancer, particularly ovarian cancer.								
CC	The present sequence represents a human ovarian carcinoma cDNA homologous								
CC	DNA.								
SQ	Sequence 5333 BP, 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;								
Alignment Scores:									
Pred. No.:	2,15e-199	Length:	5333						
Score:	2498.50	Matches:	486						
Percent Similarity:	84.09%	Mismatches:	69						
Best Local Similarity:	73.64%	Indels:	35						
Query Match:	12	Gaps:	7						
DB:									
US-10-062-879-2 (1-655) x ADM43512 (1-5333)									
OY	1 MetAlaAlaGlyValAlaAlaATrpleuProPheAlaAtgAlaAlaAlaIleGlyTrpMet	20							
D6	966 ATGGGGGGGGGTGCACGCGTGCTTTTGCAGGGCAGCGGCTATCGGGTGATG	1025							
OY	21 ProValAlaAsnCysPromcProbleuAlaProAlaAspLysAsnLYsArg---GlnAsp	39							
D6	1026 CTGTGGGCTCGGGGCTTATGCCGGCTCCCCGAGGACAGAGAAAAGACCACCAT	1055							
OY	40 GlueuileValLeuAsnValserGIyArGARphGInthrTrpARgThrThreuglu	59							

Db	1086	GCTCTCATTTGCTGAAATGATGATGGACCGGCTTCCAGACGTGGACGACACCTTGGAA	1145
QY	60	ArgTyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThr	79
Db	1146	CGTTAAACCAGACACTCTACTGCGAGATTCTGAGAGGGACTTTTCTACACACCGAAGAACT	1205
QY	80	LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg	99
Db	1206	CAGCAGATATTTCTTTGACCGGTGACCGACACATCTTCGGCCACATCTCGAAATTTTACCGC	1265
QY	100	ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla	119
Db	1266	ACTGGAAAGCTCCACTATCTCCGACGAGAGCATCTCTGCTTACGATGAAGAACTGGCC	1325
QY	120	PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArg	139
Db	1326	TTCTTTGGCCCTCATCCCGAATATATGCGCAGCTGCTTATGAGAGTACAAAGATCGC	1385
QY	140	LysArgGluAsnAlaGluArgLeuMetAspAsnAspSerGluAsnAsnGluSer	159
Db	1386	AGCGAGAGGAAGCGCCGAGCGCTCGACGACCGGATACCGACACCGCTGGGAGAGGC	1445
QY	160	--MetProSerLeuSerPheArgGlnThrMetCysThrArgAlaPheGluAsnProHisThr	178
Db	1446	GCCCTTGGCCCAACATGACTGCMAAGGCAAGGGTCTCGAGGGCTTCGAGAAACCCCAACCC	1505
QY	179	SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle	198
Db	1506	AGCAGCATGAGCCCTCGGTGTTCTACTATGTACGSGGGTTTTCATCGCTCTGTATC	1565
QY	199	ThrAsnValValGluThrValProCysGlyTyrValProGlySer---LysGluLeuPro	217
Db	1566	GCGAATGGTGGGAAACAGTGCCGTGGGATACGACCGAGTCACTTAAAGAACTGCC	1625
QY	218	CysGlyGluValGlyTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe	237
Db	1626	TGTGGAGAGCGGTATGCTGTGGCCCTTCTTCGTGTGACACAGGCTCGCATATCTTC	1685
QY	238	ThrValGluTyrLeuLeuArgLeuPheAlaIleProSerArgTyrArgPheIleArgSer	257
Db	1686	ACAGTGGATGATTTTGCTTCGCTTCGCTGGCTGGACGCGCTAGTCGTTTGTGCGATG	1745
QY	258	ValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThr	277
Db	1746	GTCATGAGTATCATCGACGTGTGGCCATCTGCTTATTCATTGGGCTGTGATGACA	1805
QY	278	AsnAsnGluAspValSerGlyValaPheValThrLeuArgValPheArgValPheArgIle	297
Db	1806	GACATGAGGACGTCAGCGGAGGCTTTGTCCACATCCGAGCTTCGGGCTTCAGAGATC	1865
QY	298	PheLysPheSerArgHisSerSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys	317
Db	1866	TTTAAAGTTTTCGCGCACTCTCAAGGCTCGGACATCTGGGGTACACACTGAAGATTGT	1925
QY	318	AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr	337
Db	1926	GCCCTCAGAAATGGGCTTCTGCTTTCGCTACCAATGGTATCATCATCTTGCGTACA	1985
QY	338	ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer	357
Db	1986	GTTATGTGTTCTACGACGAGAGAGGGCTTCTTCGCTACGAAATTCACACAGATCCCTGACCC	2045
QY	358	PheTyrPyrThrTrpIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr	377
Db	2046	TTCTGGATACCAATGTCATCCATACACATCACTAAGGATGTGTGATGATGATGCTCAAAAC	2105
QY	378	IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu	397
Db	2106	ATAGAGAGGAAGATTTTGTGTTATCTATCTGCTGCTGATGGGGCTTGGTGTCATGCTTA	2165
QY	398	ProValProValIleValSerAsnPheSerArgIleTyrHisGluAsnGluArgAlaAsp	417

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D 2166 CTTGTTCCGGTGAATGTGATTCACACTTCAGTCGATCTACACGAGATTCACGAGAGAC 2225
Q 418 Lysaargargalaglnlylsylsalaargleualargyleargvalalalythrlyser 437
D 2226 AAACGAAGGGGACAAAAGAAAGCTAGACTGGCCAGGATCCGGGACGCCAAAAGCGGAAC 2285
Q 438 SerAsnAlaTyrLeuHisSerLyAspArgAsnGlyLeuLeuAsnGlnLalaLeuGluLeuThr 457
D 2286 GCAAAATGCTTAACATGACAGCAAAAGGAAATGTTTACTCTCAATATACAGCTGACG--TCC 2342
Q 458 GlyThrProGluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477
D 2343 TCAGAGATGAGACAGCGCTTTGTTGAGCAATCCGGCTCCAGCTTTGAAACCAGACAC 2402
Q 478 HisLeuLeuHisCysLeuGlnLysThrThrGlyLeuSerTyrLeuValAspProLeu 497
D 2403 CACCTGCTTCACTGCTCGGAAAAAACACG----- 2432
Q 498 LeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGluGlnMetPheGlu 517
D 2433 -----AATCAGAGTGTGTGACGAAACAAAGCTTTGAA 2465
Q 518 GlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSer 537
D 2466 GAAGCGTCATGAGAAAGTTGCACTGTAATCGTCTTCAAGTCACAGTCTCTCACTGCT 2525
Q 538 SerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysLysThrThrHisLeu 557
D 2526 TCACACAAAGGAGACACCAACCACTGCTGTTCAAGACACAAACAACTTTTCCGAC 2585
Q 558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHis 577
D 2586 CCAATATGCCAATGATATGAGAAAGCCATCAAGTATGATACAAAGCACTCAGACGATTCAG 2645
Q 578 IleGlnLysArgGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLysAla 597
D 2646 ATCAGATGTGTGAGAGAAACACCTCTCTTAACAGCCGATCCAGTTTAAATGCCAAATG 2705
Q 598 AspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleIleSerIle 617
D 2706 GAAAGATGTGTAACTAACTGTAACCAACTTATGTACTACAGCAATATATATACATC 2765
Q 618 ProThrProProAlaLeuThrProGluGluGluSerArgPro-----ProProAlaSer 635
D 2766 CCAACACCTCCAGTACACCAACCAAGGAGAGACGATGGCAAGATCCCTGAGTACTCA 2825
Q 636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerValLeu 655
D 2826 GGAAGA-----AATATGTGACAGATTCTGCTTTC 2855
```

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PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.
PR 02-OCT-2001; 2001US-00970966.
XX (CORI-) CORIXA CORP.
XX
XX Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;
XX WPI, 2004-051070/05.
XX P-PSDB; ADM43520.
XX
XX New isolated polymucleotide encoding an ovarian tumor protein for use in
XX diagnosing, preventing or treating cancer, particularly ovarian cancer.
XX Claim 1; SEQ ID NO 254; 220pp; English.
XX
XX The invention relates to an isolated polymucleotide. The invention is
XX used to diagnose, prevent or treat cancer, particularly ovarian cancer.
XX The present sequence represents a human ovarian carcinoma CDNA homologous
XX DNA.
XX
XX Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2,15e-199 Length: 5333
XX Score: 2498.50 Matches: 486
XX Percent Similarity: 84.09% Conservative: 69
XX Best Local Similarity: 73.64% Mismatches: 70
XX Query Match: 73.23% Indels: 35
XX DB: 12 Gaps: 7
XX
XX US-10-062-879-2 (1-655) x ADM43514 (1-5333)
Q 1 MetAlaAlaGlyValAlaAlaTyrProPheAlaArgAlaAlaAlaIleGlyTyrMet 20
D 966 ATGGCGGGGGGGGTGGACGCTGCTGCTTTTCAGAGGGAGCGGCTATCGGGTGGATG 1025
Q 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg--GlnAsp 39
D 1026 CCTGGGCGCTGGGGGCTATGCGGCTCCCGCGAGGAGGAGAGAAAGACCCAAAGAT 1085
Q 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTyrArgThrThrLeuGlu 59
D 1086 GCTTCATTTGCTGAATGATGAGGCCGCCGCTTCCAGAGTGGACAGACCTCTGAA 1145
Q 60 ArgTyrProAspThrThrLeuGluGlySerThrGluLysGluPhePheAsnGluAspThr 79
D 1146 CGTTACCAAGACACTTACTGCGGCACTTCTGAGAGGAGCTTTTCTACACCCAGAAACT 1205
Q 80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99
D 1206 CAGCAGTATTTCTTTGACCGTGAGCCAGACATCTTCCGCCACATCCGAAATTTCTACCGC 1265
Q 100 ThrGlyLysLeuHisTyrProArgTyrGluLysIleSerAlaTyrAspAspGluLeuAla 119
D 1266 ACTGGAAAGCTTCATATCTTCGCGCAGAGGACATCTCTGTTACGATGAAGAACTGGCC 1325
Q 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArg 139
D 1326 TTCTTTGGCTCATCCCGGAATCATCGGCACTGCTTATGAGAGTACAAAGATCGC 1385
Q 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSer 159
D 1386 AGCGAGAGAAAGCGCGAGCGCTGAGGACGACCGGATACCGACCGCTGGGAGAGGC 1445
Q 160 ---MetProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThr 178
D 1446 GCCTTGCCCATATACGCAAGGACAGGAGGCTTGGAGGAGGCTTTCGAAACCCCAACCC 1505
Q 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
D 1506 AGCAGATGGCCCTGGTGTCTTACTATGTCAAGGGGTTTTCATGCGGCTCTGTATC 1565
```



CC is useful for treating heart failure in a subject. This sequence  
 CC represents one of the genes whose expression may be altered by the  
 CC compounds detected by the screen of the invention.

XX Sequence 5333 BP; 1509 A; 1136 C; 1167 G; 1521 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.:	2,15e-199	Length:	5333
Score:	2498.50	Matches:	486
Percent Similarity:	84.09%	Conservative:	69
Best Local Similarity:	73.64%	Mismatches:	70
Query Match:	73.23%	Indels:	35
DB:	12	Gaps:	7

US-10-062-879-2 (1-655) x ADP21361 (1-5333)

QY 1 MetAlaIaGlyValAlaIaATrPLeuProPheAlaArgAlaAlaIleGlyTPrMet 20  
 Db 966 ATGGCGGCGGGGTGGCGAGCTGGCTCTTTGGCAAGGCGACGGCTATCGGGTGGATG 1025  
 QY 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg--GlnAsp 39  
 Db 1026 CCGTGGCCCTCGGGGCTTATGCCGGCTCCCCGAGGAGAGAGAAAGAACCCAAAGAT 1085  
 QY 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59  
 Db 1086 GCTCTCATTTGCTCGAATGAGAGGACCCGCTTCAGACGTCGAGACACCCCTGGAA 1145  
 QY 60 ArgTrpProAspThrLeuLeuGlySerThrGluGlyLeuPhePheAsnGluAspThr 79  
 Db 1146 CGTTACCCAGACACTACTACGGGAGATTCTGAGAGGACCTTTTCTACCAACCCAGAAACT 1205  
 QY 80 LysGluTrpPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99  
 Db 1206 CAGCAGATTTCTTTGACCGTGACCCAGACATCTTCGCGCAATCTCTGAAATTTCTACCCG 1265  
 QY 100 ThrGlyLysLeuHisTyrTrpProArgTyrGluCysIleSerAlaTyrAspAspGluAla 119  
 Db 1266 ACTGGAGAGCTCCACTATCTCTCGCAGAGTGCATCTCTTACATGATGAAAGACCTGGCC 1325  
 QY 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGlyGluTrpLysAspArg 139  
 Db 1326 TTCTTTGGCTCATCCCGGAATATCATCGGCACTGCTTTATGAGAGTACAGAGATCCG 1385  
 QY 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAngLysSer 159  
 Db 1386 AGCGAGAGAGAACCGCGCGCTGACAGACGACGCGATACCGACACCGCTGGGAGAGAC 1445  
 QY 160 ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThr 178  
 Db 1446 GCCTTGGCCCAACCAATGGACAGGAGGAGTCTGGAGGGCTTCGAGAACCCCCACACCC 1505  
 QY 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198  
 Db 1506 AGCAGATGGCCCTGGGTGTTCTACTATGACCGGGATTTTTCATTGGCCGCTCTGTCATC 1565  
 QY 199 ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217  
 Db 1566 GCGAATGGTGGGAAACAGTGCCTGGCATCAAGCCAGATCAACATTAAAGAACTGCCCC 1625  
 QY 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db 1626 TGTGGAGAGGGATGCTGGGCTTCTTCTGCTTGACACGGCTGCGTACGATCTTC 1685  
 QY 238 ThrValGluTrpLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257  
 Db 1686 ACACTTAGATTTTCTTCTGCTGGCTGACAGCCCTTACGTTACCTTTTGGCGTAGT 1745  
 QY 258 ValMetSerIleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
 Db 1746 GTATAGATATCATCGAGTGGTGGCATCTGCTTATTATCAATGGGCTGGGATGAC 1805  
 QY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297

Db 1806 GACATGAGAGCGTACGGAGCCTTTGTCACTCCGAGTCTTCGGGCTTCAGATC 1865  
 QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317  
 Db 1866 TTTAAGTTTCCCGCACTCTCAAGGCTGGGATCTCTGGGGTACACATGAAAGATTGT 1925  
 QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
 Db 1926 GCTTCAGAAATGGGCTTCTGCTTTTCTGCTCAACATGGCTATCAACATCTTCGCTACA 1985  
 QY 338 ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357  
 Db 1986 GTTATGTTTCCGAGAGAGAGGATCTTCGCTGACAGTTCCACACATCTTCGACGCC 2045  
 QY 358 PheTrpTyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377  
 Db 2046 TTCTGTATATCATCTGTCATCATCAACAACACTAGAGTATGATGATCATGTGGCCAAATCC 2105  
 QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
 Db 2106 ATAGCAGGAGAAATTTTGGTTCTATCTGTTCTGCTGAGTGGGGCTTGGTCAATTGCTCTA 2165  
 QY 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGluAsnGlnArgAlaAsp 417  
 Db 2166 CCGTTCCGGATGTTGTTATCCAACTTCATGTCATCTTACCAACCGAATCAACGACGAC 2225  
 QY 418 LysArgArgAlaGluLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437  
 Db 2226 AAACGAGAGGACAAAGAAAGTACGTCGCGAGATCCGGGACGCAAAAGGGGAAAGC 2285  
 QY 438 SerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
 Db 2286 GCAATGTCTTACAGCAGAGCAAGCAAGAAATGGTTTACTCGATATCACTGGCAG--TCC 2342  
 QY 458 GlyThrProGluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHis 477  
 Db 2343 TCAGAGATGACAGGCTTTGTTAGCAAAATCCGGCTTCAGCTTGAACCCAGACACAC 2402  
 QY 478 HisLeuLeuHisCysValLeuGlyLysThrThrGlyLeuSerTyrLeuValAspAspProLeu 497  
 Db 2403 CACCTGCTTCACTGCTGGAAAAAACACG----- 2432  
 QY 498 LeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGluGluMetPheGlu 517  
 Db 2433 -----AATACAGATTGGAGCGAACAAGCTTTTGAA 2465  
 QY 518 GlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSer 537  
 Db 2466 GAAGCTCAGTGAAGATTGGCACTGTTATGCTCTTCATGATCAAGTCTTCACTGTCT 2525  
 QY 538 SerHisProGlyLeuThrThrCysCysSerArgArgSerLysLysThrThrHisLeu 557  
 Db 2526 TCACAAACAAGAGTACACGACACTGCTTTCAGACGACACAAAAAATCTTTCGCATC 2585  
 QY 558 ProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHis 577  
 Db 2586 CCAATATGCAATGTATCAGAGAACGATCAAGCTGTATCAAGAACTCAGACCATTCAG 2645  
 QY 578 IleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAla 597  
 Db 2646 ATCAATGTGTGGAGAGAACCTCTGTCTAACAGCGATCAATTTAAATGCCAAATATG 2705  
 QY 598 AspAspGlyLeuArgProAsnCysLeuThrSerGlnIleThrThrAlaIleIleSerIle 617  
 Db 2706 GAAAGATGTGTTAAACTAACTGAACAACCTTATGATTAAGCAATATAAGATC 2765  
 QY 618 ProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAlaSer 635  
 Db 2766 CCAACACCTCCAGTAAACACACAGAAAGAGACATAGGCGACAGATCCCTGAGTACTCA 2825  
 QY 636 ProGlyProAsnThrAsnIleProSerIleThrSerLeuValLysValSerValLeu 655



DB	2826	GGAGCA	-----	AAATATGTCAGAGTTCTGCTTGG	2855
RESULT	18				
ID	AAH21246				
XX	AAH21246 standard, cDNA; 2711 BP.				
AC	AAH21246;				
XX					
DT	13-SEP-2001 (first entry)				
XX					
DE	Human Kv4.1 cDNA.				
XX					
KM	Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;				
KM	neurodegenerative disease; ischemia; stroke; Alzheimer's disease;				
KW	Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;				
KW	learning capacity; protein kinase activator; anti-arrhythmic; ss.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	CDS	84..2024			
FT		/*tag= a			
FT		/product= "Kv4.1 alpha subunit"			
XX					
PA	DE19963612-A1.				
XX					
PD	12-JUL-2001.				
XX					
PF	29-DEC-1999; 99DE-01063612.				
XX					
PR	29-DEC-1999; 99DE-01063612.				
XX					
XX	(GENI -) FORSCHUNGSGESELLSCHAFT GENION MBH.				
DR	WPI: 2001-426637/46.				
DR	P-PSDB; AAB86318.				
PT					
PT	New potassium channel subunit proteins, useful for identifying and				
PT	testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological				
PT	agents.				
XX					
XX	Claim 11; Page 13-16; 50pp; German.				
XX					
CC	This invention describes a novel potassium channel protein (I) that is				
CC	either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium				
CC	channels containing (I) are used to identify and test: (i) compounds for				
CC	treatment of neurodegenerative diseases (autism, epilepsy, ischemia,				
CC	stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac				
CC	arrhythmia, or those that improve learning capacity and memory; and (ii)				
CC	activators of protein kinases. Host cells that express (I) can identify				
CC	agents that do not interact significantly with channels and control I to				
CC	(a quickly activated transient current), so lack the side effects of I to				
CC	known anti-arrhythmic agents. They also eliminate, or reduce, the need				
CC	for testing on organ cultures				
XX					
SQ	Sequence 2711 BP; 528 A; 867 C; 737 G; 579 T; 0 U; 0 Other;				
Alignment Scores:					
Pred. No.:	2,22e-167	Length:	2711		
Score:	2113.00	Matches:	430		
Percent Similarity:	75.07%	Conservative:	79		
Best Local Similarity:	63.42%	Mismatches:	115		
Query Match:	61.93%	Indels:	54		
DB:	4	Gaps:	14		
US-10-062-879-2 (1-655) x AAH21246 (1-2711)					
OY	1 MetalaalagivalaalaatrppeuPropehaalAARGalaaalaaaleGlyTrpmet 20				
DB	81 ATGGGCGGAGGCGTGCACGCTGGCTTTTGTCTGGGCGACGACGCTGGCGCTG 140				
OY	21 ProValAlaAsnCySPromecProleuAlaProAlaAspLyASnLyArgGlnAspGlu 40				

Db	141	CCCGTGGCGCAGCAACCCCTGCCCCCGGCACCGGGGGTGAAGGACATTCGAGGAGATGAG	200
OY	41	Leu1LeuValLeuAsnValSerGlyValArgArgPheGlnThrTPAArgThrThreLeuGluArg	60
Db	201	GTTCGTGGTGGTGAACGTGAGCGGACCGGGCTTTTGAAGATTCGGAAGAAATACCTGGACCGC	260
OY	61	TyrProAspThrLeuLeuGlySerThrGluValGlnPhePhePheAsnGluAspThrIlys	80
Db	261	TACCCAGACACCTTGCTGGGCGAGCTCGGAGAAAGAAATTTCTTACAGATCGTGACTCAAGC	320
OY	81	GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr	100
Db	321	GAGTACACTCTTCGATCGGAGACCTCGACATGTTCCGCCATGTGCTGAATCTTCTACCGAAGC	380
OY	101	GlyIysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe	120
Db	381	GGGGGGCTGCATTCGCCACCGCAGAGAGTGCATCCAGGCGCTTCGACGAGAGACTGGCTTTC	440
OY	121	TyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrIlyAspArgIlys	140
Db	441	TACGGCTCGTTCGCCAGCTAGTGGTGACTGCTGCTTGAAGATATCGGACCCGAAG	500
OY	141	ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnIleuSerMet	160
Db	501	AAGAGAAATGCCGAGCGCTGGCAGAGATGAGAAGCAGAGACGCCGGGAGACGC---	557
OY	161	ProSerIleu-----SerPheArgGlnThrMetTyrPargAlaPheGluAsnPro	176
Db	558	CCAGCCCTGCAGAGAGGAGCTCCCTGGGCGAGCGGCTTGCGGGGCTTCGAGAAATCCA	617,
OY	177	HisThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSer	196
Db	618	CACACGAGCACCGCAGCGCTCGTTCCTACTATGTGACCGGCTTCCTATCGCGCTGTCG	677
OY	197	ValIleThrAsnValValGluThrValProCys-----GlyThrValProGlySerIys	214
Db	678	GTCAATCGCAATGTGGTGAACCATCCCAATCGCGCGCTTGCCACGACGAGCTCTCAAGG	737
OY	215	GluIleuProCysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysVal	234
Db	738	GAGCAGCGCTGTGGCGAAGCGTTCACAGGCTTTTTCGTGCATGAGACAGACCGCTGTGA	797
OY	235	MetIlePheThrValGluTyrLeuLeuArgLeuPheAlaIleProSerArgTyrArgPhe	254
Db	798	CTCATATTTCACAGGTGAATACCTCTCGGGCTGTGGCCGCCACGCGGTGGCGCTTC	857
OY	255	IleArgSerValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyIleu	274
Db	858	CTGGGAGGTGCATGAGCTCATGACGTGAGTGGCCATCTGGCCCTTACTACATTTGGGCTT	917
OY	275	ValMetThrAsnAsnGluAspValSerGlyValAlaPheValThrLeuArgValPheArgVal	294
Db	918	TTGGTGGCCAAAGACGACGATGTTCTTGCGGCCCTTTGTCAACCTCGCGTGTTCGGGTG	977
OY	295	PheArgIlePheIysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrIleu	314
Db	978	TTTGGCATCTTCAAGTTCTCCAGGSCATCCACAGGGCTTGAAGATTCTGGGCTACACACTC	1037
OY	315	LysSerCysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIle	334
Db	1038	AAGAGCTGTGCTTGAGCTGGGCTTCTCTCTTTTCCCTAACCATGCGCATCATCTATTC	1097
OY	335	PheAlaThrValMetPheTyrAlaGluGlySerSerAlaSerIysPheThrSerIle	354
Db	1098	TTTGGCATGTGCATGTTTATGTCTGAGAAGGGCAGAAACAGACCACTTTACAAAGCATC	1155
OY	355	ProAlaSerPheTyrTyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetVal	374
Db	1158	CTCTCGGCGCTTCTGGTATACATGTGCATGCATGACCAACGCTTGGCTTCGAGGACATGGTG	1217
OY	375	ProIysThrIleAlaGlyIysIlePheGlySerIleCysSerIleuSerGlyValIleuVal	394
Db	1218	CCGAGCACCATGTGCGAGAAATTTGGGGTCATGTGCTACTACAGTGGGGGTCTGGCT	1277



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QY 395 11eAlaLeuProValIleValIleSerAsnPhseSerArgIleTyrHisGlnAsnGln 414
1278 ATTGCCCTGCTGTCAGCATTTGTCACAACTTACCGCATCTACACAGAAACAG 1337
QY 415 ArgAlaAspIleArgIleArgIleValIleValIleValIleValIleValIle 434
1338 CGGCTGACAAAGCGGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1397
QY 435 ThrGlySerSerAsnAlaTyrIleHisSerIleArgAsnGlyLeuLeuAsnGlnAlaLeu 454
1398 AGTGTACCAACCAATGCTTCTCCAGTACAGCAATGAGG-----GGCCTT 1445
QY 455 GlnLeuThrGlyThrProGlnGlnGlnIleMet--GlyValThrThrSerLeuIleGln 473
1446 GAGGACACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1505
QY 474 SerGlnHisHisIleLeuLeuHisCysLeuGlnGlnGlnThrThrGlyLeuSerTyrLeuVal 493
1506 CAGCAACATCACCACTTGCTGCACTGTCTAGAGAAAGCAAG----- 1547
QY 494 AspAspProLeuLeuSerValArgThrSerThrIleAsnHisGlnIleAspGln 513
1548 -----TGCATGATGATTCACAGATGAG 1568
QY 514 GlnMetPheGlnGlnAsnGlyMetGlnSerSerMetGlnAsnTyrProSerThrArgSer 533
1569 CTCACCTTCAGTGAA--GCCCTGGAGAGCGCTCCGCGGCTGGCCGACACAGCCGTAGC 1625
QY 534 ProSerLeuSerSerHisBPro-----GlyLeuThrThrThrCysCysSerArg 549
1626 ACCTGTGTGTCTTCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1685
QY 550 ArgSerIleYs--LysThrThrHisLeuProAsnSerAsnLeuProAlaThrArgLeuArg 568
1686 AGGGCCAGAGGCGCGGCGCATCCCGCTTGCCCACTCCAGTCCCTCAGTCAAGCCGT---GGC 1742
QY 569 SerMetGlnGlnLeuSerThrIleHisIleGlnGlySerGlnProSerLeuThrThr 588
1743 AGCATGAGAGAGGTGAGCATG-----CTGGCAGGGGCTGGCGAGAGCATGCCCTCAG 1796
QY 589 SerArgSerSerLeuAsnLeuValAlaAspArgGlyLeuArgProAsnGlySerThrSer 608
1797 AGCGGCTCCAGCCTCATGCAAGCCCATGACAGCCTTGAACCTGCAACCTGCAACCCGG 1856
QY 609 GlnIleThrThrAlaIleIleSerIleProThrProProAlaLeuThrProGlnGlyGln 628
1857 GACTTGTGCTGCTGCATTTACAGATCCCTTACCCCTCTCTGCCAACCACCCAGAT---GAG 1913
QY 629 SerArgProProProAlaSerProGly----- 637
1914 AGCCAA-----CCTTCCTCCCTGGGCGGCGGTGGAGGCGCGGAGCAGCCTCAGAGAAC 1967
QY 638 ProAsnThrAsnIleProSerIleThrSerAsnValValIleValSerValLeu 655
1968 TCCAGCCTGGTACCCCTTGTCCCGGAGAGCTGTCAAGATTCATCCCTG 2021

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## RESULT 19

AAZ11901 standard; cDNA; 3424 BP.

```

ID AAZ11901
XX AC AAZ11901,
XX DT 30-NOV-1999 (first entry)
XX DE Human potassium channel K-Hnov12 cDNA.
XX KM Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
XX KM cardiovascular disorder; CNS disorder; renal disorder; ds.
OS Homo sapiens.
XX Key Location/Qualifiers
FH

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FT CDS 257..2195
FT FT /*tag= a
FT FT /product= "Human K-Hnov12 potassium channel"
FT FT /note= "No stop codon given in specification"
FT FT /transl_except= (pos:375, aa:Glu or Gly)
FT FT replace(321,T)
FT FT /*tag= b
FT FT replace(407,C)
FT FT /*tag= c
FT FT variation
FT FT MO9943696-A1.
PD 02-SEP-1999.
PF 22-FEB-1999; 99WO-US003826.
PR 25-FEB-1998; 98US-0076687P.
PR 07-AUG-1998; 98US-0095836P.
PR 19-JAN-1999; 99US-0116448P.
XX (AXYS-) AXYS PHARM INC.
XX PA Miller AP, Curran ME, Hu P, Rutter M, Wang J;
XX PI WPI, 1999-527591/44.
XX DR P-PSDB; AAY34123.
XX PS New nucleic acids encoding mammalian K-Hnov potassium channel proteins,
XX PS useful for the diagnosis and treatment of episodic ataxia with myokymia,
XX PS cardiac arrhythmia, epilepsy and Bartter's syndrome.
XX PS Claim 4; Page 57-60; 112pp; English.
XX
XX This sequence represents human potassium channel K-Hnov12 cDNA. K-Hnov
XX proteins have a high degree of homology to known potassium channels and
XX may be alpha subunits, which form the functional channel, or accessory
XX subunits that act to modulate the channel activity. K-Hnov12 is a voltage
XX gated potassium channel. The gene's chromosomal location is Xp21,
XX determined via PCR chromosomal localisation using primers AAZ11926 and
XX AAZ11927. K-Hnov cDNAs were isolated by extension of expressed sequence
XX tags (ESTs) which were related but not identical to known human potassium
XX channels. Potential polymorphisms detected as sequence variants between
XX multiple independent clones. Potassium channels have critical roles in
XX various cell types and biochemical pathways. Defective potassium channels
XX are known to cause four human diseases: episodic ataxia with myokymia;
XX cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
XX As potassium channels are critical components of virtually all cells, it
XX is likely that abnormal potassium channels are also implicated in certain
XX renal, cardiovascular and central nervous system (CNS) disorders.
XX CC Nucleotides encoding K-Hnov proteins may be used for identifying
XX CC homologous or related proteins and the DNA sequences encoding them. They
XX CC may be used to produce compositions that modulate the expression and
XX CC function of the K-Hnov protein and in studying the biochemical pathways
XX CC associated with it. They may also be used for the recombinant production
XX CC of K-Hnov protein in fermentation cultures. Additionally, such
XX CC nucleotides may be used in gene therapy protocols for the treatment of
XX CC diseases associated with abnormal potassium channels
XX
XX SQ Sequence 3424 BP; 680 A; 1081 C; 887 G; 775 T; 0 U; 1 Other;

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## Alignment Scores:

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Pred. No.: 1.78e-166 Length: 3424
Score: 2104.00 Matches: 429
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Query Match: 61.66% Indels: 54
DB: 2 Gaps: 14

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US-10-062-879-2 (1-655) x AAZ11901 (1-3424)

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QY 1 MetaAlaAGIValAlaAlaTTrpLeuProPheAlaArgAlaAlaAlaIleGlyTyrMet 20
DB 257 ATGGCGGAGAGCGCTGGCCAGCGTGTGCTTGTCTGGGAGGAGGAGGAGGAGGAGGAGG 316

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OY	21	ProValAlaIaenCyPmeMeProleuAlaProAlaAspIysAsnLysAlaArgLysAspGlu	40
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OY	41	LeuLeValLeuAsnValSerGlyAArgArgPheGlnThrTrpArgThrThrLeuGluArg	60
Db	377	GTTCGTGTGTGAACGTAGCGGAGCGCCCTTGAACCTTGGAAAGAAATACGTCGACCC	436
OY	61	TyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThrLys	80
Db	437	TACCAGACACCTTCTGGCGAGCTCGAGGAAGAAATCTTCTACGATCTGACTCAGGC	496
OY	81	GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr	100
Db	497	GAGTACTTCTTCGATCGGACCTTCACATGTTCCGCACATGTGCTAACTTCAACCGAACG	556
OY	101	GlyLysLeuHisTyrProArgTyrGlyCysIleSerAlaTyrAspAspGluLeuAlaPhe	120
Db	557	GGCGCGGCTGCATTTGCCACGGAGGAGTGCAATCCAGGCTTTCAGAAAGAGCTGGCTTTC	616
OY	121	TyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArgLys	140
Db	617	TACGGCTCGTTCCCGAGCTAGTCGTGACTCTCTCCCTTGAAGATATCGGACCGAAG	676
OY	141	ArgGluAsnAlaGluArgLeuMetAspAsnAspSerGluLysAsnGlnIuSerMet	160
Db	677	AAGGAGAAATGCCGACCGCTGGCAAGATGAGAGAGACAGACAGCGCGGAGACGAC--	733
OY	161	ProSerLeu-----SerPheArgGlnThrMetTrpArgAlaPheGluAsnPro	176
Db	734	CCAGCCCTGCACGAGGAGAGCTCCCTGGCGAGCGGCTCTGGCGGGCTTCAAGATCA	793
OY	177	HisThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSer	196
Db	794	CACACGAGCACCGGAGCCCTCTGTTTCTACATGATGACCGGCTTCTTCAATCGCCGTGTC	853
OY	197	ValIleThrAsnValValGluThrValProCys-----GlyThrValProGlySerLys	214
Db	854	GTCATCGCAATGTGTGGAGACATCCATCCATCCGGGCTCTGCACGAGGTCCTCAAG	913
OY	215	GluLeuProCysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysVal	234
Db	914	GAGCAGCCCTGTGGGAAAGCTCTCCACAGGCGCTTTCGTGATGAGACAGCCGTGTGA	973
OY	235	MetIlePheThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPhe	254
Db	974	CTCAATTTACAGCGTGAATATCTCTCGGGCTGTTTGCCGCCCAAGCGCGTTCGCGCTTC	1033
OY	255	IleArgSerValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGluLeu	274
Db	1034	CTGGGAGTGTATAGCTCTACATCAACGTGTGGCGCATTCCTGCTACTACATTTGGGCTT	1093
OY	275	ValMetThrAsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgVal	294
Db	1094	TTGGTGCCCAAGAAACGAGATGTCTGTGGCGCTTGTATCACTCGATGTGTTCCGGGNG	1153
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Db	1214	AAGACGTGTGCTCTGAGCTGGAGCTTCTCTCTTTCCTTACCAATGGCATTCATCATC	1273
OY	335	PheAlaThrValMetPheTyrAlaGluLysGlySerSerAlaSerLysAspPheThrSerIle	354
Db	1274	TTTGCACATGTCATGTTTATATGCTGTGAAGGAGCAAAACAAAGACCACTTTCAAGCATC	1333
OY	355	ProAlaSerPheTrpTyrThrIleValThrMetThrThrLeuGlyTyrGlyLysPheVal	374
Db	1334	CTGTGGGCTTCTGTGATATCAATGTGCACATGACCAACGCTGTGGCTACGGAACATGGTG	1393

[illegible]





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 13, 2005, 11:52:53 ; Search time 4528.18 Seconds  
(without alignments)  
5505.991 Million cell updates/sec

Title: US-10-062-879-2  
Perfect score: 3412  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database :  
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3: gb\_hlc.\*  
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6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	3278.5	96.1	1911	9	AY419309 Mus muscu
3	3103.5	91.0	1911	9	AY419308 Pan trogl
4	2549	74.7	3730	3	AK033962 Mus muscu
5	2503.5	73.4	2997	3	AK032268 Mus muscu
6	2399.5	70.3	1893	9	AY406814 Mus muscu
7	2391.5	70.1	1893	9	AY406812 Homo sapi
8	2122	62.2	1956	9	AY408065 Mus muscu
9	2113	61.9	1944	9	AY408063 Homo sapi

10	1693.5	49.6	1893	9	AY406813 Pan trogl
11	1607	47.1	1939	9	AY408064 Pan trogl
12	1532	44.9	3302	3	AK033805 Mus muscu
13	1317.5	38.6	1054	9	CNS03211 Tetradon
14	1270.5	37.2	993	9	CNS0590A Tetradon
15	1209.5	35.4	997	9	CNS02DRX Tetradon
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17	1033	30.3	628	8	BZ020918 CH230-390
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19	988	29.0	695	1	AL120075 DKEPDP761M
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22	928	27.2	567	4	BI033106 MR4-NM020
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24	915.5	26.8	698	5	BM947382 UI-M-BGDP
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26	891	26.1	903	9	CNS02CAE Tetradon
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28	840	24.6	715	6	CB167795 FBB603000
29	837	24.5	662	9	CE336550 ligR-gss-
30	824.5	24.2	612	5	BO340099 MR4-NM020
31	823	24.1	509	2	BF399610 UI-R-CAO-
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36	748.5	21.9	477	7	CR790592 DKEPDP459M
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38	747	21.9	2565	9	AY417318 Homo sapi
39	745	21.8	463	6	CD804043 UI-M-GVO-
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43	713.5	20.9	1572	9	AY400869 Homo sapi
44	713	20.9	1758	9	AY398826 Homo sapi
45	712.5	20.9	2146	3	BC023222 Mus muscu

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ACCESSION	AY419307				Genomic survey sequence.
VERSION	AY419307.1				GI:39775264
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D., and Cargill,M.				1 (bases 1 to 1911)
AUTHORS	Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D., and Cargill,M.				
TITLE	Infering nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science	302 (5652),	1960-1963	(2003)	
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1911)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D., and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003)				
COMMENT	Rockville, MD 20850, USA				
FEATURES	These sequences were made by sequencing genomic exons and ordering them based on alignment.				
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 Query Match: 96.47% Indels: 19  
 Gaps: 1

US-10-062-879-2 (1-655) x AY419307 (1-1911)

QY 1 MetAlaAlaGlyValAlaAlaATrPLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet 20  
 Db 1 ATGGCGGCGCGAGTGGCGCTGGCTGCTTTTGGCCGGGCTGCGGCATCGGGTGGATG 60  
 QY 21 ProValAlaAlaAsnGlyPheMetProLeuAlaProAlaAspLysAsnLysArgGlnAspGlu 40  
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 QY 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGluArg 60  
 Db 121 CTGATTCTCTCAACGTGAGTGGGGCGGAGGTTCAGACCTGGAGGACCAAGCTGGAGGCC 180  
 QY 61 TyrProAspThrLeuLeuGlySerThrGlnLysGluPhePheAsnGluAspThrLys 80  
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 Db 241 GAGTACTTCTTCAACCGGAGACCCGAGGTGTCCGGCTGCGCTCAACTTCAACCCAG 300  
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 QY 201 ValValGluThrValProCysGlyThrValProGlySerIleGluLeuProCysGlyGlu 220  
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VERSION AY419309.1  
KEYWORDS GI:39775266  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1911)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 1911)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
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US-10-062-879-2 (1-655) x AY419309 (1-1911)

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DEFINITION	Pan troglodytes KCND3 gene, VIRUAL TRANSCRIPT, partial sequence,			
ACCESSION	AY419308			
VERSION	AY419308.1	GI:39775265		
KEYWORDS	SSS.			
SOURCE	Pan troglodytes (chimpanzee)			
ORGANISM	Pan troglodytes			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.			
TITLE	1 (bases 1 to 1911)			
JOURNAL	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,			
PUBMED	Todd,M.A., Tenenbaum,D.M., Ciyello,D.R., Lu,F., Murphy,B.,			
AUTHORS	Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,			
TITLE	Adams,M.D. and Cargill,M.			
JOURNAL	Direct Submission			
COMMENT	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,			
FEATURES	Rockville, MD 20850, USA			
	These sequences were made by sequencing genomic exons and ordering			
	them based on alignment.			
	Location/Qualifiers			

Source	1..1911
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 LOCUS  
 DEFINITION  
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 ACCESSION  
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 VERSION  
 AK033962.1 GI:26329580  
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 HTC, CAP trapper.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
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 1  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 MEDLINE  
 PUBMED  
 10349636  
 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20493974  
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 11042159  
 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, E., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
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 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
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 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
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 Nature 420, 563-573 (2002)  
 6 (bases 1 to 3730)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirazane, T., Hori, P., Imctani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),



**TITLE**  
JOURNAL

**COMMENT**

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Satou, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sato, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://phantom.gsc.riken.jp/.  
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**CDS**

**FEATURES**  
**SOURCE**

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Gaps: 3	7

US-10-062-879-2 (1-655) x AK032268 (1-2997)

**ORIGIN**

Alignment Scores:  
Spec. No.:  
Pred. No.:  
Score:  
Percent Similarity:  
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 QY 199 ThrAenAenValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217  
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 QY 218 CysGlyGluArgTrpSerValAlaPhePheCysLeuAenAenAenAenAenAenAenA 237  
 DB 1642 TGTGGGGAGAGTGTGGGTGCTTCTTGTGATGATGATGATGATGATGATGATGATGAT 1701  
 QY 238 ThrValGluTrpLeuAenAenAenAenAenAenAenAenAenAenAenAenAenAenA 257  
 DB 1702 ACAGTGTGATGCTGTGCTGCTGCGCGACCATGATGATGATGATGATGATGATGATG 1761  
 QY 258 ValMetSerIleIleAenValAlaIleMetProTrpTrpIleGlyLeuValMetThr 277  
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 QY 278 AenAenGluAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 297  
 DB 1822 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1881  
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 DB 1882 TTTTAAAGTTTCCCGCCACTCTCAAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1941  
 QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
 DB 1942 GCATTCAGACATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2001  
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 DB 2002 GTTATGTTCTTACGAGAGAGAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2061  
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 QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValIleAenValIleAlaLeu 397  
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QY 398 ProValProValIleValIleValIleValIleValIleValIleValIleValIleVal 417  
 DB 2182 CCGGTGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTG 2241  
 QY 418 LysArgGluAenAenAenAenAenAenAenAenAenAenAenAenAenAenAenAen 437  
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 DB 2302 GCAATGTGCTTACATGAG 2358  
 QY 458 GlyThrProGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 477  
 DB 2359 TCGGAGATGAAACCGGCTTATGAGCAATGTGATGAGCTTGTGAGACAGACACAC 2418  
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 DB 2482 GAATGCTGTGAG 2541  
 QY 538 SerHisProGlyLysLeuThrThrCysCysSerArgArgSerLysLysThrThrHisLeu 557  
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 QY 558 ProAenSerAenLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHis 577  
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 DB 2662 ATCAGATGTGTGAG 2721  
 QY 598 AenAenGlyLysLeuArgProAenCysLysThrSerGlnIleThrTrpAlaIleIleSerIle 617  
 DB 2722 GAGAGGTGTGTTAACTTAACTGATGAGACACCTTACGATGAGACACATTAATAGATC 2781  
 QY 618 ProThrProProAlaLeuThrProGluGlyLysSerPro-----ProProAlaSer 635  
 DB 2782 CCAACACCTCCAGTAAACACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2841  
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 DB 2842 GGAGGA-----AATATGTCAGAGGTGTCTGCTTG 2871  
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 LOCUS Mus musculus KCOND2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AY406814  
 VERSION AY406814.1 GI:39762785  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1893)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tamendau,D.M., Cavello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302



QY 578 ILeGInGlySerGIuGInPProSerLeuThrThrSerArgSerSerLeuAenLeuYsala 597  
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QY 598 AspAspGlyLeuArgProAenCysLysThrSerGlnLeuThrThrAlaIleIleSerIle 617  
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Db 1801 CCAACACCTCCAGTAAACACCCAGAGCGGACGAGCCGAGTCTCCTGAGTATTCG 1860  
QY 636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValValIysValSerValIleu 655  
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RESULT 7  
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DEFINITION genomic survey sequence.  
ACCESSION AY406812  
VERSION AY406812.1 GI:39762783  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1893)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1893)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
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Score: 2391.50 Matches: 469  
Percent Similarity: 80.76% Conservative: 64  
Best Local Similarity: 71.06% Mismatches: 92  
Query Match: 70.09% Indels: 35  
DB: Gaps: 6

US-10-062-879-2 (1-655) x AY406812 (1-1893)

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Db 1 ATGGCGGGGGGGGGGGGGCTGCTCTTTTCAAGGCGAGGGCTATCGGGTGGATG 60  
QY 21 ProValAlaAenCysProMetProLeuAlaProAlaAspIysAsnIysArg---GlnAsp 39  
|||||  
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Db 61 CCTGGGCTCGGGGGCCTATGCCGGCTCCCCAGAGAGAGAGAAAGCAACAGAT 120  
QY 40 GlnLeuIleValIleAenValSerGlyArgArgPheGlnThrTrpArgThrLeuGlu 59  
Db 121 GCTCTATGCTGCGAATGTAGATGGACCCGCTTCCAGACGTGGACACCCCTGGAA 180  
QY 60 ArgTrpProAspThrLeuLeuGlySerThrGlnIysGlnPhePheAsnGluAspThr 79  
Db 181 GGTACCCAGACACTCTACGTGGGCGAGTCTGAGAGGACCTTTTCTACACCCAGAACT 240  
QY 80 LysGlnIyrPhePheAspArgAspProGluValPheArgCysValIleAenPheTrArg 99  
Db 241 CAGACGATATTTCTTGAACCGTGACCCAGACATCTTCCGCCACATCCGAAATTTCTACGC 300  
QY 100 ThrGlyIysLeuHsIyTrpProArgTrpGluCysIleSerAlaTrpAspAspGluLeuAla 119  
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QY 120 PheTrpGlyIleLeuProGluIleIleGlyAspCysGlyTrpGluGlyIysAspArg 139  
Db 361 TCTTGGCTCTATCCCGAAATATCATGCGACACTGCTGTATAGAGATCAAGAGATGCG 420  
QY 140 LysArgGlnAenAlaGluArgLeuMetAspAspAsnAspSerGluAenAenGlnGluSer 159  
Db 421 AGCGAGAGAAAGCGCGAGCGCTGACAGAGACGCGGATCCGACACCGCGGGAGAGCG 480  
QY 160 ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThr 178  
Db 481 GCCTTGCACCAACAGACTGCAAGAGAGGTCTGAGAGGCGCTTCGAAACCCCAACCC 540  
QY 179 SerThrLeuAlaLeuValPheTrpTrpValThrGlyPhePheIleAlaIleSerValIle 198  
Db 541 AGCAGATGCGCCCTGGTGTCTTACTATGTCAAGGGAGTTTTCATTCGCTCTGTATC 600  
QY 199 ThrAenValAlaGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217  
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QY 218 CysGlyGluArgTrpSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
Db 661 TGTGAGAGCGGATGTGCTGTGGCTTCTTCTGCTTGGACACGGCGCTCGCATATCTTC 720  
QY 238 ThrValGluTrpLeuLeuArgLeuPheAlaAlaProSerArgTrpArgPheIleArgSer 257  
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QY 258 ValMetSerIleIleAspValAlaIleMetProTrpTrpIleGlyLeuValMetThr 277  
Db 781 GTCATGATATCATGACGTGTGGCCATCTGCTTATTAATTTGGGCTGTGATGACA 840  
QY 278 AsnAenGluAspValSerGlyValaPheValThrLeuArgValPheArgValPheArgIle 297  
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QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTrpThrLeuLysSerCys 317  
Db 901 TTTAAGTTTCCCGCACTTCAGAGCGCTGTGCATCTCGGGGTACACATGAAGAGTTGT 960  
QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
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QY 338 ValMetPheTrpAlaGluIysGlySerSerAlaSerIysPheThrSerIleProAlaSer 357  
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QY 358 PheTrpTrpThrIleValThrMetThrThrLeuGlyTrpGlyAspMetValProLysThr 377  
Db 1081 TTCTGTATACCATGTGTACCATGTACCAACATTAAGGTATGTGACATGTGTCCAAAAC 1140  
QY 378 ILeAlaGlyIysIlePheGlySerIleCysSerLeuSerGlyValIleValIleAlaLeu 397  
Db 1141 ATAGAGGAGAGATTTTGGTTCTATCTGTTCTGCTGAGTGGGGCTTGGTATTTGCTCTA 1200







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Db      598 GTGATTGCCAAGCTCGGAGACCATCCATGCTGCTGATACCCACAGATGCCCTCCAA 657
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      658 GAGCAGAGCTGTGTGTGACCGCTTCCCTACAGACCTTTTCTGTATGACAGACGCTGTGTA 717
Qy      235 MetIlePheThraValGluYrIleuLeuAargLeuPheAlaAlaProSerArgYrAargPhe 254
      718 CTATATTTCAAGAGGAGATACCTGCTGCGCTCTTGCGACGCCCGCGTGTGCTTC 777
Qy      255 IleArgSerValMetSerIleIleAapValAlaIleMetProYrYrIleGlyLeu 274
      778 CTGCGAGGTGTGATGACCTTATCGATGTGTGCGCATCTTACCTACTATATATGGGCTG 837
Db      275 ValMetThraAanGluAapValSerGlyAlaPheValThraLeuValPheArgVal 294
      838 TTGCGTCCCAAGATGATGATGCTGTGCTGCTTGTCACCTCGTGTGTTCCGGATC 897
Qy      295 PheArgIlePheLeuPheSerArgHlaSerGlnGlyLeuAargIleLeuGlyYrThraLeu 314
      898 TTCGATCTTCAAGATCTCAGGACATCGCAGGCGCTGAGATCTGAGGTACACCTTC 957
Qy      315 LysSerCysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThraAlaIleIleIle 334
      958 AAGAGCTGTGCTGTGAGCTGAGCTTCTCTCTTCTTCCCTACAGTGGCATCATCATC 1017
Db      335 PheAlaThraValMetPheYrAlaGluLeuGlySerSerAlaSerIlePheThraSerIle 354
      1018 TTTCGCACCTGCTCATGTTCTATGCTGAGAGAGGCGACGAGAACCACTTCAACAACATC 1077
Qy      355 ProAlaSerPheTrpYrTrpIleValThraMetThraIleuGlyYrGlyAapMetVal 374
      1078 CTGCTGCTCTTCTGTGATACCATTTGTCACATGACCACTTGAGTGTGAGATGATGTA 1137
Qy      375 ProIleThraIleAlaGlyIlePheGlySerIleCysSerLeuSerGlyValLeuVal 394
      1138 CTAAGACCATGTGAGGCAAAATTTGGGTCCATCTGCTACCTTACGCGGTGCTTGTC 1197
Db      395 IleAlaLeuProValProValIleValSerAapPheSerArgIleYrIleGlnAanGln 414
      1198 ATTGCTTGTGCTGCGAGCATGATGATCAACTTCACTGACGCGCATTCACAGAACAG 1257
Qy      415 ArgAlaAapIleAargAlaGlnLeuValAlaArgLeuAlaArgIleAargValAlaArg 434
      1258 CGTCTCTACAGACCCCGGCGACAGCAAAAGTGGCTGCGCAAGATCCCTTTGGCAAG 1317
Qy      435 ThcGlySerSerAanAlaYrIleuHlaSerIleArgAanGlyLeuLeuAanGluAlaLeu 454
      1318 AGTGTATCCACCAATGCTTCTCTGCACTATAGCAAAATGGG-----GGCTTC 1365
Db      455 GtuleuThraGlyThraProGluGluGlnIleMet---GlyYrThraThraSerIleGlu 473
      1366 GAGACAGATGGCAGTGGCGACGCAAAATGCTGTGAGAGCGCTCTGCTTTGAA 1425
Qy      474 SerGlnIleHlaIleLeuLeuHlaCysLeuGlnIleYrThraGlyLeuSerYrLeuVal 493
      1426 CAACAGATCAACCATCTGCTGCACTTGTCTGAGAAAGCTCG----- 1467
Qy      494 AapAapProLeuLeuSerValArgThraSerThraIleYsAanHlaGluPheIleAapGlu 513
      1468 -----TGTACGAGTTCAACAGACAG 1488
Qy      514 GlnMetPheGlnAanCysMetGluSerSerMetGlnAanYrProSerThraArgSer 533
      1489 CTAACTTTAGATGAGGCGCTTGAGAGATCTCACTGGAGTGGTGGCACACAG---CGAGT 1545
Qy      534 ProSerLeuSerSerIlePro-----GlyLeuThraThraCysCysSerArg 549
      1546 ACCTCAATATCATCCAAACCAATGGGCGTGGAGCGCTTCTCATCTCTGCTCGA 1605
Qy      550 Arg---SerIleYsIleThraIleuProAanSerAanLeuProAlaThraArgLeuArg 568
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Qy      589 SerArgSerSerLeuAanLeuValAapAapGlyLeuArgProAanCysIleYrThraSer 608
      1717 ACCGCTTAACCTCTCAATGCCAGACCCACAGACGCTTACCTGAACTGATGACAGCCGG 1776
Qy      609 GlnIleThraAlaIleIleSerIleProThraProAlaLeuThraProGluGly 628
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      1834 AGTCAACCTTCTCCCTCAGTGTGTGTGGCGAGGTGTGGACACACCAACACATCTC 1893
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LOCUS      Homo sapiens KCND1 gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION      genomic survey sequence.
ACCESSION      AY408063
VERSION      AY408063.1 GI:39764034
KEYWORDS      GSS.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1944)
      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
      Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
      Adams,M.D. and Cargill,M.
      Interfering nonneutral evolution from human-chimp-mouse orthologous
      gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
AUTHORS      2 (bases 1 to 1944)
      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
      Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
      Adams,M.D. and Cargill,M.
      Direct Submission
TITLE      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
      Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
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Score:      2113.00      Matches:      430
Percent Similarity:      75.07%      Conservative:      79
Best Local Similarity:      63.42%      Mismatches:      115
Query Match:      61.93%      Indels:      54
DB:      9      Gaps:      14

US-10-062-879-2 (1-655) x AY408063 (1-1944)
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Qy      41 LeuLeValIleuAenValIserGlyArgArpGheGlnThrTrpArgThrThreGluArg
Db      121 GTTGTGGTGGTGAACGTGAGCGACCGGCGCTTTGAGACTTGAAAGAAATACCTGGAGCCG
Qy      61 TyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThrLys
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Qy      81 GluTyrPhePheAspArgAspProGluValPheArgCysValIleuAenPheTyrArgThr
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Qy      101 GlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe
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Qy      161 ProSerLeu-----SerPheArgGlnThrMetTrpArgAlaPheGlnAspPro
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Qy      177 HisThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSer
Db      538 CACACGACGACCGGAGCCCTGTTTCTATGATGACCGGCTTCTCATATGCGCGTGC
Qy      197 ValIleThrAsnValIleGluThrValProCys-----GlyThrValProGlySerLys
Db      598 GTCATCCCAATGTGTGAGACCATCCATGCCGCGCTGCACGACGAGTCTCTCAAG
Qy      215 GlnLeuProCysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysVal
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Qy      235 MetIlePheThrValIleGluTyrLeuLeuArgPheAlaIleProSerArgTyrArgPhe
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Qy      255 IleArgSerValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeu
Db      778 CTGGAGAGTGTCAATGAGCTCATCGATGCTGTGGCAATCTGCCCTACTACATTGGGCTT
Qy      275 ValMetThrAsnAsnGluAspValIserGlyAlaPheValThrLeuArgValPheArgVal
Db      838 TTGGTGGCCCAAGAACGATGTCTGTGGCGCTTGTGCACCTTGCCTGCGGTTCGGGTG
Qy      295 PheArgIlePheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeu
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Qy      315 LysSerCysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIle
Db      958 AAGAGCTGTGCTGTGAGCTGGCTTCTCTCTTTCCTTAACATGAGCCATCATCATC
Qy      335 PheAlaThrValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIle
Db      1018 TTTCGCCCTGTCATGTTTATGCTGAGAAAGGCGCAAAAGCAAGCAACTTTCAAAGCATC
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Db      1138 CCCAGCACACATTTGCTGGCAAGATTTTGGGTTCCATCTGTCTCATCTCATGTGGGCTTGGTC
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Db      1198 ATTGCCCTGGCTGGCCAGTATGTTGTCCAACTTTAGCCGATCTACACACAGAACAG
Qy      415 ArgAlaAspLysValArgAlaGlnLysValAlaArgLeuAlaArgIleArgValAlaLys
Db      1258 CGGGCTACAAAGCCCGACAGCAGACAGAGAGGTGGCTTGGCAAGATCCGATCCGATCAAG
Qy      435 ThrGlySerSerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeu
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Db      1366 GAGGACAGCGGCACTGGCGAGAAACAGGCTTTGTGTACAGAAACCGTTCGCTTGA 1425
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Qy      494 AspAspProLeuLeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGlu
Db      1468 -----TGCATGAGTTTACAGATGAG 1488
Qy      514 GlnMetPheGlnGlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSer
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Qy      534 ProSerLeuSerSerHisPro-----GlyLeuThrThrThrCysCysSerArg
Db      1546 ACCTGTGTCTTCCAGCAGAGTGGAACCGGAAGCCGTGTGTCTTGTGCTGCTGCTG
Qy      550 ArgSerLys---LysThrThrHisLeuProAsnSerLysLeuProAlaThrArgLeuArg
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Qy      589 SerArgSerSerLeuAsnLeuLysAlaAspAspGlyLeuArgProAsnCysLysThrSer
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## RESULT 10

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LOCUS Pan troglodytes KCND2 gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406813
VERSION AY406813.1 GI:39762784
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

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REFERENCE 1 Mammalia: Eutheria; Primates; Catarrhini; Homiidae; Pan.  
AUTHORS 1 (bases 1 to 1893)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 1893)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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Best Local Similarity: 53.94% Mismatches: 216  
Query Match: 49.63% Indels: 35  
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Db 1 ATGGCGGCGGGGCTGGGCGAGCGTGGCTCTTTTGCAAGACACGGCTATCGGGTGAATG 60  
QY 21 ProValAlaAsnCySPrometProLeuAlaProAlaAspIysAsnIysArg--GlnAsp 39  
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QY 40 GlnLeuIleValIleuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59  
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QY 60 ArgTyProAspThrIleuLeuGlySerThrGluIleGluPhePhePheAsnGluAspThr 79  
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QY 100 ThrGluIleuLeuHisTyRProArgTyRGlucyIleSerAlaTyRAspArgGluAla 119  
Db 301 ACTGGGAAGCTCCACTATCTCGGACAGAGTGCAATCTCTTACGATGAAGAACTGGCC 360  
QY 120 PheTyRGlYIleLeuProGluIleIleGlyAspCySerTyRGlugu-----TyRlys 137  
Db 361 TTTCTTGGCTTCATCCCGAAATCANNNGACAGCTGTTATGAGGAGTANNNNNNNNNN 420  
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QY 158 GluSerMetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHis 177

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QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr 337  
Db 961 GCCTCAGAAATTNNNNNTCTCTCTTCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020  
QY 338 ValMetPheTyRAlaGluIysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357  
Db 1021 NNN 1080  
QY 358 PheTrpTyRThrIleValThrMetThrThrLeuGlyTyRgluAspMetValProLysThr 377  
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QY 378 IleAlaGlyValIlePheGlySerIleCysSerLeuSerGlyValIleuValIleAlaLeu 397  
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QY 398 ProValProValIleValSerAsnPheSerArgIleTyRHisGlnAsnGlnAspArgAla 417  
Db 1201 CCGGTTCCGGATTTGATCCAACTTCAGTGCATCTACCAACCAATCAACGAGCAGAC 1260  
QY 418 LysArgArgAlaGlnIysValAlaArgLeuAlaArgIleArgValAlaIysThrGlySer 437  
Db 1261 AAACGAAGGCGCAAAAGAAAGCTAGACTGSCAGATCCGGGCGCAAAAGCGGAAGC 1320  
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QY 458 GlyThrProGluGluGluHisMetGlyTyRThrThrSerLeuIleGluSerGlnHis 477  
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QY 498 LeuSerValArgThrSerThrIleLysAsnHisGluPheIleAspGluGluMetPheGlu 517  
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QY 518 GlnAsnCyMetGluSerSerMetGlnAsnTyRProSerThrArgSerProSerLeuSer 537

Db 1501 GAAAGCTGCATGAGATTGCAACTGTTAATGCTCTTCAAGTCAAGTNNNCACTGTCT 1560  
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Qy 636 ProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerValLeu 655  
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LOCUS Pan troglodytes KCND1 gene, VIRUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY408064  
VERSION AY408064.1 GI:39764035  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
REFERENCE 1 (bases 1 to 1939)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 1939)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
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1. 1939  
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Percent Similarity: 61.39% Conservative: 66  
Best Local Similarity: 51.63% Mismatches: 207  
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Qy 1 MetAlaIaGlyValAlaAlaIlePleuProPheAlaArgAlaAlaIleGlyTrpMet 20  
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Db 421 NNN 480  
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Qy 196 SerValIleThrAsnValIleGluThrValProCysGlyThrValProGlySerLysGlu 215  
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      1777 GACTTCGTGGCTGCATATACAGATCCCTACCTCCTGCAACACCCAGATGNNAG 1836
Db      629 SerArgProProAlaSerProGly-----637
Qy      1837 CAA-----CCTTCTCCCTCCGCGCGGCGTGGCAGGCGCGGACACCTTCAGAAC 1887
Qy      638 ProAnThrAnIleProSerIleThrSerAnValValLysValSer 653
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RESULT 12
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LOCUS AK033805
DEFINITION Mus musculus adult male epididymis cDNA, RIKEN full-length enriched
library, clone:9230112B12 product:potassium voltage-gated channel,
Shal-related family, member 1, full insert sequence.

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ACCESSION AK033805
VERSION AK033805.1 GI:26329482
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitamura, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Onara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagata, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imocani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohato, N.,
Okazaki, Y., Saio, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/

```







REFERENCE	
AUTHORS	1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzames,C., Winkler,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE	Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE	20296633
PUBMED	10835645
REFERENCE	2
AUTHORS	Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C., Fitzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL	Genome Res. 10 (7), 939-949 (2000)
MEDLINE	20359837
PUBMED	10899143
REFERENCE	3 (bases 1 to 993)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES	Location/Qualifiers
SOURCE	1..993 /organism="Tetraodon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone="O5IG22" /clone_1ib="A" /note="Genoscope sequence ID : COAA05IBD11AI-end : T3"
ORIGIN	
Alignment Scores:	
Pred. No.:	1..41e-109                  Length:                  993
Score:	1270..50                   Matches:                   248
Percent Similarity:	91.30%                   Conservative:               25
Best Local Similarity:	82.94%                   Mismatches:               25
Query Match:	37.24%                   Indels:                   4
DB:	Gaps:                     1
US-10-062-879-2 (1-655) x CNS059DA (1-993)	
Dy	71 LysGluPhePhePheAsnGluAspThrLysGluTyRPhePheAspArgspProGluVal 90
Dd	988 AAAGANTTTTTTTTNAACGAGAGGGCAAGNGTACTTTTTTGACCGGGATCCGATGCC 929
Dy	91 PheaArgCysValLeuAsnPheTyArgThrglyLysLeuHisrYrProArtyrGlyCys 110
Dd	928 TTCAGGAACATCTTCACCTTYTACCAGCGGMAAGCTTCANTACCTTCGCACAGACGTGC 869
Dy	111 IlleSerAlaTyRAspAspGluLeuAlaPheTyrglyIleLeuProGluIleIlleGlyAsp 130
Dd	868 ATCTCAGCTTAGATGACGAGNTGACATTCTTCGCACTATCATCCAGACTCATCGCGCAC 809
Dy	131 CysCyTyrgluglutyLyAspArgLySaArgLuAsnaIagUargLeuMetAspAsp 150
Dd	808 TGCTGCTACGAAAGGTAACAAGAACAAGAGGGAATTAGAGCGGCTCGAGAGTAT 749
Dy	151 AsnAspSerGluAsnAsngIngluSerMetProserLeuSerPheArtyrGlnThrMetTrp 170
Dd	748 CAGGAG--GAGAAACAAGACACCAAGAGTCCCCAACATGAACCTTAGGCAACCAATGGG 692
Dy	171 ArgAlaPheGluAsnProHsrThrserrThryleuAlaValAlaPheTyrTyValThrGly 190
Dd	631 CGCGCTTTGAGAACCCCAACCACTTCACACATGAGCGCTGTCTTATATTAAGTCAAGGT 632
Dy	191 PhePheIleAlaValSerValIleThrasnValValGluThrValProCyGlyThrVal 210

Df		631	TTCTTCATCCGACATGGTGCATCACCAAGTGAGGAGCGGTGCC-TGGGTTTCAAG	573
Oy		211	ProgliserlysgluleuProCyeglygluarqfyrservValAlaphePheCylueuAsp	230
Df		572	GCCAATGAAGAAGACGTCCGTGTGAGAGCGCTACACGGTGGGCTTCTTCGATGCAC	513
Oy		231	ThrAlaCyValMetLilepheThrValGlunryrleuenuAgyLeuPheAlAlProser	250
Df		512	ACGGCTGCGGAATCTTACAGTGAAGTACTGATGCCCTGTGTGCGCGCTTAAC	453
Oy		251	ArgTyraArgPheileArgrSerValMetSertelleaspValAlalleMeProtyr	270
Df		452	CCTAACCGCTTAAAGCGCTCGGTATAGCATCATTAACGTGAAGGCCATCTGCCCTAC	393
Oy		271	TyrilleglyLeuValMetThrAsnAsngluAspValSerGlyAlapeValThrleuarg	290
Df		392	TACATTGGCTTGGTAGATACCACAAGAGAGAGCGGCGCTTCGN-TNCNTGGCG	334
Oy		291	ValPhearValPheaaglllePheLyPheSerArghIserrgInglyLeuArglleu	310
Df		333	GTCTTCGCGCTTCCGATCTTCAAGTTCCTCCGCACTCGACGGGCTGGCGATCTGT	274
Oy		311	GlyTyrrhleuLysserCyAlaSerGluenucllyPheleuPheSerLeuThmet	330
Df		273	GGCTACAGCGTCAAAG-TCGCGCTCGAGGTGGGCTTCCTGCTTCTCCTTACATG	215
Oy		331	AlallellellePheAlaThrValMeCPheTyralgluLysglySerSeraIAseryls	350
Df		214	GCCATCATCATCTTCGCCACCGCTATGTTTACCGGAGAAAGATCATCAGTCCAGCAAG	155
Oy		351	PheThrSerllePleaIAserPheTyrrTyrrThlleValThrMetThrleuugly	369
Df		154	TTTACACAGTATCCCGGCTTCTTGTGATACATATTGTGACTATGACAACACTG3GG	98
RESULT 15				
CNS02DRX/c				
LOCUS				
DEFINITION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
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TITLE				
JOURNAL				
MEDLINE				
PUBMED				





Df		3	GTCATCGCCCTGCCCCGTTCGGTACATGCATTGCCAACTTGAGCGCATGTAOCACCAAGAAC	62
Oy		414	GLNARGALAAAPLYSARGARGALAGLNYLSYSAIARGLEUALAARGYLAEARGVALA	433
Df		63	CAGCGTCGCCGACAAGCGCGGGGACAGAAGAAAGCTCGCGTCCGAGAGATCCGCGTGCC	122
Oy		434	LysThrnglySerSerAsnAlaTyrlLeuhisSerLySaArganGlylLeuLeuanGlnAla	453
Df		123	AAGACAGGACACTCCAAATGCTCATTCTGACACAGCAAACCAACGAGCTCTGAACCAACC	182
Oy		454	LeugluLeuThrngly---ThrgluGlnGluunHismetGlyLygThrThrsertleule	472
Df		183	CTCGAGCTGACGGGATGCCATGAGATGAACAGCATACAGCTMAAGCACCTCTTAATT	242
Oy		473	GluserglnHisshileuleunhisCyseulglynlysthrnglyleusertyleu	492
Df		243	GAAAGCCAATCATCACCACTGCTGACAGCTCGAAAAAACAACCGAGTTGCTCATCTT	302
Oy		493	ValasparProleulleuservAlarghrserThrillelysashihGluPhelasp	512
Df		303	GTGATGTATCCCCTGTTATCTGTAGAACTTCACATCAAGAACACAGATGTCAATAAT	362
Oy		513	GIUglImetPegluGlnAsnCysmetGlusersermetGlnastTyProserThrarg	532
Df		363	GAGCAACTGTTTCGACACAGACTGCATGAGAGACTMAATGCAAAATTACCTCTTCGG	422
Oy		533	SerProserleuserserHisProglyLeuthrThrCySeSerArgserlys	552
Df		423	AGCCCTCTCTGTCAAGTACCAAGCGCTGACCACTCTGCTGTCTTCGGCGTCAAG	482
Oy		553	LysThrThrHisleuProasnserAsnleuProalathrArgleuArgsermetGlnu	572
Df		483	AAGACCAACACACTTCCCAACTCCGACGCTGCACAGCTACCCGCTCCGACATGACGAG	542
Oy		573	LeuserrThrIleHisIleGlnGlyserGlnGlnProserleuThrThrsertserSer	592
Df		543	CTCAGCACCATTCACATTCACAGGCAGTAGACAGCCCTCACTTACACCAAGTGTCTCAGT	602
Oy		593	LeuasnleuLySAIAASPspolyLeuargrProasnCySLysThrsertGlnlethrThr	612
Df		603	CTCAACATGAANTCAGATGATGGCTGGACCGAActGCAAAAGCCGCCAATMACACA	662
Oy		613	AlaIleIleSerlleProThrProProalaLeuthrProGluGlyGlusertArgProPro	632
Df		663	GCCATCATCAACATCCACACGCCGCGCGCTCACACAGAAAGGAGAGACAGACTCG	722
Oy		633	ProhaserProGlyProasnThrAsnIle---ProserIleThrSeranValvally	651
Df		723	CCCGACACCCCCGGGCACTCCACGAAACATTTCTACACACACACACACACATCATGTCAA	782
Oy		651	sValserValleu 655	
Df		783	GGTCTCTGCTTG 795	
RESULT 17				
LOCUS	BZ203918	628 bp	DNA	linear GSS 11-OCT-2002
DEFINITION	CH230-390612_TV CHORI-230 Segment 2 Rattus norvegicus genomic clone			
ACCESSION	BZ203918			
VERSION	BZ203918.1 GI:23861970			
KEYWORDS	GSS.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.			
REFERENCE	1 (baes 1 to 628)			
AUTHORS	Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,P., de Jong,P. and Fraser,C.M.			
TITLE	Rat BAC End Sequences from Library CHORI-230 MboI segment			
JOURNAL	Unpublished (1999)			

COMMENT	Other GSSs: CH230-390G12.TU Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdf@tigr.org) Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or) ering information.htm). BAC end page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html Plate: 390 row: G column: 12 Seq primer: T7 Class: BAC ends.									
FEATURES	Location/Qualifiers									
source	1..628 /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="BN/SMNsd/MCW" /db_xref="taxon:10116" /clone="CH230-390G12" /sex="Female" /cell_type="Brain" /clone_1ib="CHORI-230 Segment 2" /note="Vector: pTRABAC1.3; Site 1: MboI; Site 2: MboI; CHORI-230 Rat (BN/SMNsd/MCW) BAC library produced by Pieter de Jong"									
ORIGIN										
Alignment Scores:										
Pred. No.:	2.36e-87									
Score:	1033.00									
Percent Similarity:	98.09%									
Best Local Similarity:	97.13%									
Query Match:	30.28%									
DB:	8									
	Gaps: 0									
US-10-062-879-2 (1-655) x BZ203918 (1-628)										
QY	129	GIYAAPCYG	YRTYRG	UGIURTY	YSAPAGLY	YARG	GLUNASNA	LAGLUA	GLEUMET	148
DB	2	GGCGACTGCTGCTATGAGAGATCAATAC	-CCCAAGCGGAGAACCTGAGCGGCTCATG	60						
QY	149	ASAPASAPASAPSERGIUNASNA	ANGINGUSERMET	PROSER	LEUSER	PHEAR	GTGINTHR	168		
DB	61	GATGACAAATGATCTGAGAACAA	CCAGGATCATG	CCCTCC	TACAGCTT	CGCCAGAC	120			
QY	169	METTPAR	GAALAPHG	GIUNAS	PROHIS	THRSER	THLEUAL	ALEUVAL	PHETRYT	VAL
DB	121	ATGTGGCGGGCTT	TGAGAAC	CCACACAC	ACACAG	CCCTGG	ACTGCTT	CTTACT	AGTG	180
QY	189	THRGY	PHAPHEIL	LEALAV	ALSERVAL	IIETHR	ASNAVAL	VALGIU	THRVAL	PROCYSGLY
DB	181	ACAGGCTTCTT	CATTGCGGCT	CGGATCAC	CCAAAGT	GTGAGAC	CGGTGCC	ATCGGC	240	
QY	209	THRV	ALPROG	LYSER	GLUL	LEUPROCYSGI	YGIU	ARGTYR	SERVAL	ALAPHEPCYS
DB	241	ACGGGCTCGGGAG	CAGAGAAC	CTGCCGT	TGAGAG	CGGCTAC	CTCCGTGG	CTTCTT	CTGC	3000
QY	229	LEU	ASPTHR	ALACYS	VALMET	IIEPHE	THRVAL	GIUTYR	LEUL	LEUARG
DB	301	CTGGAC	ATCGCTGT	GTCTAT	GAATCTT	CACGGT	AGAT	ACTCTC	CTCG	ACTCTT
QY	249	PRO	SER	ARGTYR	ARGPHEIL	LEARG	SERVAL	MET	SER	IIEL
DB	361	CCCA	CAGAGT	ACCGCTT	CATCCG	CAGT	GTGATG	AGCAT	CGAC	CGTGGT
QY	269	PRO	TYR	TYR	II	LEU	VAL	MET	THR	ASNA
DB	421	CCCT	ATAT	CAAT	GTGG	CTGT	ATGAC	CAAC	ACAG	GAAG

QY 289 LeuArgValPheArgValPheArgIlePheIysPheSerArgHisSerGlnGlyLeuArg 308  
 DB 481 CTCGGGCTCTCCGCGCTCTCAGAGATCTCAAGTCTCCCGCATTCACGAGGCTACCG 540  
 QY 309 IleLeuGlyThrThrLeuIysSerCysValAspGluLeuGlyPheLeuIlePheSerIleu 328  
 DB 541 ATCTTAGGCTACACCTCGAAGAGCTGGCTCAAACTAGGCTTCTCTCTCTCTCTC 600  
 QY 329 ThrMetAlaIleIleIleIlePheAlaThr 337  
 DB 601 ACCATGGGCTATCATCTTGGCACT 627  
 RESULT 18  
 CO393575 723 bp mRNA linear EST 01-JUL-2004  
 LOCUS AGENCOURT 26755085 NIH MGC 255 Rattus norvegicus cDNA clone  
 DEFINITION IMAGE:7321104 5', mRNA sequence.  
 ACCESSION CO393575  
 VERSION CO393575.1 GI:49575491  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 723)  
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Daniela S. Gerhard, Ph.D.  
 COMMENT Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bidg. 31 Rm10A07 Bethesda, MD 20892  
 Email: gcgabs-remail.nih.gov  
 Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical  
 College of Wisconsin  
 cDNA Library Preparation: Express Genomics  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHM15384 row: g column: 22  
 High quality sequence stop: 690.  
 Location/Qualifiers  
 1. 723  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="IMAGE:7321104"  
 /sex="both"  
 /tissue\_type="Brain - Pooled from several tissues from one  
 or more individuals"  
 /lab\_host="DH10B Tona"  
 /clone\_id="NIH\_MGC\_255"  
 /note="Organ: brain/CNS; Vector: pExpress-1; Site 1:  
 EcorV; Site 2: NotI; RNA obtained from brain tissue of 8  
 wk old animal. Tissues were snap-frozen and kept at -80C  
 before RNA extraction and purification (Tri-reagent  
 method). cDNA was primed using oligo-dT primer:  
 5'-pGACTAGTCTTAGATCGAGCGCGCCGCC(T)25-3' and cloned into  
 the EcorV/NotI sites of pExpress-1. Size-selection >1.25kb  
 resulted in an average insert size of 1.7 kb. This primary  
 library is a normalized (primary library is NIH MGC 254)  
 and was constructed by Express Genomics (Frederick, MD).  
 Note: this is a NIH\_MGC library"  
 ORIGIN  
 Alignment Scores: 4.95e-84 Length: 723  
 Pred. No.: 999.00 Matches: 199  
 Score: 83.46% Conservative: 18  
 Percent Similarity:

Best Local Similarity: 76.54% Mismatches: 23  
 Query Match: 29.28% Indels: 20  
 DB: 7 Gaps: 2  
 US-10-062-879-2 (1-655) x CO393575 (1-723)  
 QY 294 ValPheArgIlePheIysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyThr 313  
 DB 3 GCTTCAGAGATCTTAAAGTTTCCGCGCACTCTCAAGGCTGGGATACCTGGGATACACA 62  
 QY 314 LeuIysSerCysValAspGluLeuGlyPheLeuIlePheSerIleuMetAlaIle 333  
 DB 63 CTGAAGAGCTGTGCTGAGAACTGGCTTCTTCTCTTCCCTCAAGAGGCTATCATC 122  
 QY 334 IlePheAlaThrValMetPheTyraIleGlyIysSerAlaSerIysPheThrSer 353  
 DB 123 ATTTTCGCTACGGTTATGTTTACGACAGAGAGGCTCTCAGACCAAGTTTCAACAGC 182  
 QY 354 IleProIysSerPheThrPyrThrIleValThrMetThrIleuGlyTyraIysMet 373  
 DB 183 ATCCCTGAGGCTTCTGTATCACCATGTCATCAACATGAACTGGGATAGGACATG 242  
 QY 374 ValProIysThrIleAlaGlyIysIlePheGlySerIleCysSerLeuSerGlyValIleu 393  
 DB 243 GTACCAAAAACCATAGCAGGGAAGATTTCGGCTATCTGCTCTCTGAGCGAGCTTG 302  
 QY 394 ValIleAlaLeuProValProValIleValSerAsnPheSerArgIleTyraIleGlnAsn 413  
 DB 303 GTCATCGGCTACCCGCTGCTGATGCTGTCTTAATTCAGTCCGATCTACCAACAAAC 362  
 QY 414 GlnArgAlaAspIysArgArgAlaGlnIleIysValAlaArgLeuAlaArgIleArgValAla 433  
 DB 363 CAACAGCGGACAAACGAAAGGACACAAAGAAACGAGGCTGGCAGAGATCCGGGACGCC 422  
 QY 434 IysThrGlySerSerAsnAlaTyraIleuHisSerIysArgAsnGlyLeuLeuAsnGluAla 453  
 DB 423 AAAAGTGAATGCAAAATGCTTACATGACAGCAAGCGAATGGTTACTAGGACAAACAA 482  
 QY 454 LeuGluLeuThrGlyThrProGluGluGluHisMetGlyIysThrThrSerLeuIleGlu 473  
 DB 483 CTGCAG--TCCTGGAGAGATGAACCGGCTTCTGTAATTCGATCCAGCTTCGAG 539  
 QY 474 SerGlnHisHisIleLeuHisCysLeuGluIysThrThrGlyLeuSerTyraIleVal 493  
 DB 540 ACACAAACACCAACACCTGCTTCACTGCTGAGAAACCAAG-----581  
 QY 494 AspAspProLeuLeuSerValArgThrSerThrIleIysAsnHisGluPheIleAspGlu 513  
 DB 582 -----AACCATGAGTTTGTGATGAA 602  
 QY 514 GlnMetPheGluGlnAsnCysMetGluSerSerMetGlnAsnTyraProSerThrArgSer 533  
 DB 603 CAAGCTTTGAAGAAAGCTGCATGGAAGTGCCACTGTATTCCTTCATAGCACACAG 662  
 QY 534 ProSerLeuSerSerHisProGlyLeuThrThrCysCysArgArgSerIys 553  
 DB 663 CCTTCCTCTCTTCCCAACAGAGTCACAGCACTGCTGCTCAGAGACACAAAAA 722  
 RESULT 19  
 AL120075 695 bp mRNA linear EST 04-SEP-2003  
 LOCUS DKF2P761M132.71 761 (synonym: hamy2) Homo sapiens cDNA clone  
 DEFINITION DKF2P761M132 5', mRNA sequence.  
 ACCESSION AL120075  
 VERSION AL120075.1 GI:5925974  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 695)  
 AUTHORS Ottenweider, B., Obermaier, B., Mewes, H.W., Gaessenhuber, J. and  
 Wiemann, S.

TITLE	EST (Ottewaelder, et al.)
JOURNAL	Unpublished (1999)
COMMENT	Contact: MIPS

## FEATURES

Alignment Scores:	
Pred. No.:	5,15e-83
Score:	988.00
Percent Similarity:	92.07%
Best Local Similarity:	85.02%
Query Match:	28.96%
BB:	1
Length:	695
Matches:	193
Conservative:	16
Mismatches:	16
Indels:	2
Gaps:	1

US-10-062-879-2 (1-655) x AL120075 (1-695)

## ORIGIN

Qy		20	ThValProCys-----GlyThrValProGlySerGluLeuProCys61Vqlunrg	22
Dd		2	ACATCCCATGCCGGCGCTGTGCAGCAAGTCTCTAAGGAGAACACTCTGTGGCAAGC	61
Qy		222	TyrSerValAlaPhePheCysIleuAspTrlAlaCysValMetIlePheThrValGlnTry	24
Dd		62	TTCCCAAGGCCCTTTTTCTGCATGGACACAGCCTGTGACTATTTCACAGTGGAATAC	122
Qy		242	LeuLeuArgLeuPheAlaIalApProSarCgTyzAcPheIleArxSerValMetSerIle	26
Dd		122	CTCTGGGCTGTtTTCGCCGCCACCCTTGGCCGCTTCTCGGAGTGTATGAGCTTC	18
Qy		262	IleAspValValAlaIleMetProTyryrIleGlyLeuValMetTrnAsnGlnLasp	28
Dd		182	ATCGAGTGGTGGCCATCCGCTGACCTACTCATTTGGGCTTTTGTGCCACAAGAAGACAT	24
Qy		282	ValSerGlyValAlaPheValThrLeuArgValPheArgValPheArgIlePheIysPheSer	30
Dd		242	GTCCTGGGCGCTTTTTCACCCCTGCTGTGTTCCGGAGTTCGGATCTTAAGTTCTCC	30
Qy		302	ArgHisSerGlnGlyLeuArgIleLeuGlyTyrrThrLeuIysSerCysAlaSerGlnLeu	32
Dd		302	AGGCATCTCACAGGGCTTTGGAGANTTCGGGCTACACACTCAAGCTGTGGCTGAGCTG	36
Qy		322	GlyPheLeuLeuPheSerIleuThrMetAlaIleIleIlePheAlaThrValMetPheTyrr	34
Dd		362	GGCTTCTCTCTTTTCCCTAAACAGAGGCATCATCATTTTGGCACGTCATGTTTTAT	42
Qy		342	AlaGlnIlyesGlySerSerAlaSerIysPheThrSerIleProAlaSerPheTrityrThr	36
Dd		422	GCTGAGAGGGCACAAACAAGACCAACTTACAGACTCCGCGGCTTGGGTATACC	48
Qy		362	IleValThrMetThrThrLeuGlyTyrrGlyAspMetValProLyThrTrlIalaGlylys	38
Dd		482	ATTGTACCAATGACACGCTGTGGTACAGGACATGAGTCCACGACACATTTCTGGCAAG	54

US-10-062-879-2 (1-655) x CN220459 (1-753).

Qy	378	ILEALGIYLIYHLEPHGLYSERIIECVSESRLEUSRGIYALLIEUVAIIIEALIEU	397
Db	31	GTACACGGGAAGATCTTCGACTCCATCTGCTGACGGGGGTGCTGGTATCGCCCTG	90
Qy	398	PROVALPRVALIIIEVALSERANDHESERAGIIETRYHISGLINAMGNALASP	417
Db	91	CCGGTTCGGCATATGTCTCCAACTTCAGCGGCATCTACCAACCAAGCCAGTCCGCAC	150
Qy	418	LYSARGARGALEGLNLYSVALAARGLEUALAARGIIIEARVALALALAYSTHGLYSER	437
Db	151	AACCGCCGGGCACAGAAAGATCTGGCTTCGAGAGATCCCGTGGCCAAAGACAGCGAGC	210

**FEATURES**

**SOURCE**

Email: Peter.Savolainen@biotech.kth.se  
Seq primer: M13 reverse primer.

REFERENCE  
1 (bases 1 to 753)  
Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and

ORGANISM

RESULT	20
CN220459	
LOCUS	CN220459 753 bp mRNA linear EST 08-APR-2004
DEFINITION	RA0066A09.ab1 Rubrain Gallus gallus cdna 5', mRNA sequence.
ACCESSION	CN220459
VERSION	CN220459.1 GI:46293801
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Db 662 CAGCAGAGGTGCCCTTGCA 682

Qy 382 IllehgylserllecysserleuSERglyValleuValleuValleuProvalProval 401b

Db 542 ATTTTCGGGTCATCTGCTACTCAGTGGCGTCTTGTCATTGCCCGCCCTGTGCCAGTTC 601b

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Qy 438 SerAsnAlaTyrLeuHisSerIysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
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 Qy 458 Gly---ThrProGluGluGluHisMetGlyLeuThrThrSerLeuIleGluSerGluHis 476  
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 Qy 477 HisHisLeuLeuHisCysLeuGluIlyThrThrGlyLeuSerTyrLeuValAspAspPro 496  
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Search completed: April 13, 2005, 18:32:17  
 Job time : 4595.18 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_p2n model

Run on: April 13, 2005, 10:33:33 ; Search time 6316.65 Seconds  
(without alignments)  
4878.777 Million cell updates/sec

Title: US-10-062-879-4

Perfect score: 3320  
Sequence: 1 MAAGVAAWLPFAAAAGM.....PGPNTIPITSNVKSVL 636

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4708233 segs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Database :

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2: gb\_hlg:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3320	100.0	2064	6	AR371347 Sequence
2	3311	99.7	1911	9	AF205856 Homo sapi
3	3311	99.7	2104	6	A85164 Sequence 1
4	3311	99.7	2104	6	AR204884 Sequence

5	3304	99.5	1996	10	RN075448	U75448 Rattus norv
6	3303	99.5	1911	6	AF048712	AF048712 Homo sapi
7	3300.5	99.4	2121	6	AR371346	AR371346 Sequence
8	3298	99.3	1911	10	AF107782	AF107782 Mus muscu
9	3297	99.3	7258	10	RN142975	U42975 Rattus norv
10	3281.5	99.1	1968	6	AX956786	AX956786 Sequence
11	3291.5	99.1	1968	6	AF205857	AF205857 Homo sapi
12	3291.5	99.1	2072	6	A85166	A85166 Sequence 3
13	3291.5	99.1	2072	6	AR204885	AR204885 Sequence
14	3289	99.1	1984	9	AF187964	AF187964 Homo sapi
15	3285.5	99.0	1968	10	AF334791	AF334791 Rattus no
16	3285	98.9	2104	6	A85168	A85168 Sequence 5
17	3285	98.9	2104	6	AR204886	AR204886 Sequence
18	3284.5	98.9	1968	10	AB003587	AB003587 Rattus no
19	3283.5	98.9	1968	9	AF048713	AF048713 Homo sapi
20	3283.5	98.9	2722	10	AF120491	AF120491 Homo sapi
21	3278.5	98.8	1968	10	AF107781	AF107781 Mus muscu
22	3269.5	98.5	1968	4	AF196445	AF196445 Oryctolag
23	3269.5	98.5	2041	9	AF187963	AF187963 Homo sapi
24	3266.5	98.4	2057	4	AF454388	AF454388 Musceta p
25	3126	94.2	1977	5	AF209722	AF209722 Gallus ga
26	3055	92.0	4262	10	RATKV43R	L48619 Rattus norv
27	2873	86.5	1665	4	AF493549	AF493549 Oryctolag
28	2843.5	85.6	2840	5	XL083265	U99265 Xenopus lae
29	2590	78.0	3056	5	BC045304	BC045304 Danio rer
30	2530	76.2	2918	4	AY147192	AY147192 Musceta p
31	2524	76.0	1907	4	AF508735	AF508735 Oryctolag
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35	2518	75.8	2351	9	HSBJ10969	AJ010969 Homo sapi
36	2518	75.8	5026	10	AB093280	AB093280 Mus muscu
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#### ALIGNMENTS

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DEFINITION AR371347  
ACCESSION AR371347  
VERSION AR371347.1 GI:34608279  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2064)  
AUTHORS Cockett,M.I., Dilks,D.W., Ling,H.-P.C. and Sokol,P.T.  
TITLE Human potassium channel polynucleotide and polypeptides and uses thereof  
JOURNAL Patent: US 6395477-A 3 28-MAY-2002;  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0



TITLE Long and Short Human Isoforms of the Kv4.3 Channel: Cloning,  
Expression, Electrophysiology, Pharmacology and Phosphorylation by  
Protein Kinase C

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1911)  
AUTHORS Calmeils, T. P. G., Faivre, J.-F., Javre, J.-L. and Bril, A.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-1999) Cardiovascular Pharmacology, SmithKline  
Beecham, 4 Rue du Chesnay Beauregard, Saint Gregoire 35760, France

FEATURES  
SOURCE location/Qualifiers  
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ORIGIN

## Alignment Scores:

Pred. No.: 5,966-216 Length: 1911  
Score: 3311.00 Matches: 634  
Percent Similarity: 99.69% Conservative: 0  
Best Local Similarity: 99.69% Mismatches: 2  
Query Match: 99.73% Indels: 0  
Gaps: 0

US-10-062-879-4 (1-636) x AP205856 (1-1911)

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QY 41 LeuIleValIleAsnValSerGIyARgArpPheGlnTrTPArGThThrIleuGlnArg 60  
Db 121 CTGATTGCTCTCAAGTGAAGTGGGCGAGGTTTCAAGCTTGAAGCAACGCTGAAGGCG 180  
QY 61 TyrProAspThrIleuGlnSerThrgIuYsgIuPhePheAsnGlnuAspThrIys 80  
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QY 121 TyrGlyIleLeuProGlnIleIleGIyAspCySyTyRgIuGluTyRlyAspArgIys 140  
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QY 201 ValValGluTrnValProCySgIyThrValProGlySerLyGluLeuProCySgIyGlu 220  
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ACCESSION AB5164  
VERSION AB5164.1 GI:6733867  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2104)  
AUTHORS Brill,A.M. and Calmels,T.P.  
TITLE KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  
JOURNAL Patent: WO 9842833-A 1 01-OCT-1998;  
BRL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)  
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US-10-062-879-4 (1-636) x AB5164 (1-2104)

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 Db 1441 CACTGCCCTGGAAAAACCACTAACCAAGATTATATGATGACAGATGTTTGAGAGAAC 1500  
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 ACCESSION AR204884  
 VERSION AR204884.1 GI:21502324  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 2104)  
 AUTHORS Bril,A.Michel,Alain., Calmels,T.Paul,Gerard.,  
 TITLE Kv potassium channel polypeptides and polynucleotides  
 JOURNAL Patent: US 6368823-A 1 09-Apr-2002;  
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US-10-062-879-4 (1-636) x AR204884 (1-2104)

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 Qy 101 GlyLysLeuHISerTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
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 Baktayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 Rattus.  
 1 (bases 1 to 1996)  
 AUTHORS Dixon, J.E., Shi, W., Wang, H.S., McDonald, C., Yu, H., Wymore, R.S.,  
 Cohen, I.S., and McKinnon, D.  
 TITLE Role of the Kv4.3 K+ channel in ventricular muscle. A molecular  
 correlate for the transient outward current  
 JOURNAL Circ. Res. 79 (4), 659-668 (1996)

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MEDLINE 96428386
PUBMED 8831489
REFERENCE 2 (bases 1 to 1996)
AUTHORS Dixon, J.E., Shi, W., and McKinnon, D.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1996) Neurobiology, SUNY at Stony Brook, Life
Sciences Building, Stony Brook, NY 11794-5230, USA
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Query Match: 99.52% Indels: 0
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 REFERENCE 1 (bases 1 to 1911)  
 AUTHORS Kong, W. and Tomasselli, G.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-FEB-1998) Medicine, Johns Hopkins University School of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA  
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 Pred. No.: 3303.00 Matches: 634  
 Score:



AUTHORS Cockett,M.I., Dalks,D.W., Ling,H.-P.C. and Sokol,P.T.  
TITLE Human potassium channel polynucleotide and polypeptides and uses  
thereof

JOURNAL Patent: US 6395477-A 1 28-MAY-2002;  
Location/Qualifiers

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US-10-062-879-4 (1-636) x AR371346 (1-2121)

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LOCUS Mus musculus potassium channel Kv4.3M mRNA, complete cds.

DEFINITION AF107782

ACCESSION AF107782.1 GI:4324646

VERSION

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 1911)

AUTHORS Tanaka,H., Janzen,K., Winkfein,R.J., Fiset,C., Clark,R.B. and Giles,W.R.

TITLE Cloning and functional characterization of mouse heart K+ channel alpha subunits, Kv1.5, Kv4.2 and Kv4.3

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1911)

AUTHORS Tanaka,H., Janzen,K., Winkfein,R.J., Fiset,C., Clark,R.B. and Giles,W.R.

TITLE Direct Submision

JOURNAL Submitted (19-NOV-1998) Physiology and Biophysics, University of Calgary, 3330 Hospital Dr. NW, Calgary, AB T2N 1N4, Canada

FEATURES

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VERSION U42975.1 GI:1150862
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus
REFERENCE 1 (bases 1 to 7258)
AUTHORS Serodio, P., Vega-Saenz de Miera, E. and Rudy, B.
TITLE Cloning of a novel component of A-type K+ channels operating at
J. Neurophysiol. 75 (5), 2174-2179 (1996)
JOURNAL MEDLINE 96317227
PUBMED 8734615
REFERENCE 2 (bases 1 to 7258)
AUTHORS Serodio, P. and Rudy, B.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1995) Paulo Serodio, Department of Physiology and
Neuroscience, New York University Medical Center, 550 First Avenue,
New York, NY 10016, USA

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ORIGIN
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Best Local Similarity: 99.37% Mismatches: 2
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 REFERENCE  
 1 Kaletta, T.J., Dewulf, N.E. and Placetink, G.K.  
 Authors Methods for identifying and developing compounds that interact with  
 TITLE voltage-gated potassium channels of the Kv4 family  
 JOURNAL Patent: WO 03097682-A 4 27-NOV-2003;  
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 Qy 161 ProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThrSerThr 180  
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RESULT 11  
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 DEFINITION complete cds.  
 ACCESSION AF205857  
 VERSION AF205857.1 GI:6644151  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1968)  
 AUTHORS Calmeils T.P.G., Faivre,J.-F., Javre,J.-L., Cheval,B., Rouanet,S.  
 and Brill,A.  
 TITLE Long and Short Human Isoforms of the Kv4.3 Channel: Cloning,  
 Expression, Electrophysiology, Pharmacology and Phosphorylation by  
 Protein Kinase C  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1968)  
 AUTHORS Calmeils T.P.G., Faivre,J.-F., Javre,J.-L. and Brill,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-1999) Cardiovascular Pharmacology, Smithkline  
 Beecham, 4 Rue du Chesnay Beaurgard, Saint Gregoire 35760, France  
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Db 1801 CTGAGACCAAACTGCAAAATCCCAATCATCACAGCATCATCATCATCCCACTCC 1860  
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Db 1861 CCAGCCCTAACCCCAAGAGGGGAAAGTCGGCCACCCCTGCGACCCAGAGCCCAACAG 1920  
Qy 622 AsnIleProSerIleThrSerAsnValValIleValSerValLeu 636  
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DEFINITION Sequence 3 from Patent WO9842833.  
ACCESSION A85166  
VERSION A85166.1 GI:6733868  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2072)  
AUTHORS Bril,A.M. and Calmels,T.P.  
TITLE KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  
JOURNAL Patent: WO 9842833-A 3 01-OCT-1998;  
BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)  
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Oy		441	TyrLeuHissSerLysArgAsnGlYleuLeuAnsiuaLeuGluleThrGlYthrPro	460
Db		1331	TACTTCGACAGCAGACCAGCGGGCTCTTCAACAGAGGGCTGGAGTACGGGCACCCCA	1380
Oy		461	GlugluginJHismetGlYlvsThrThrserLeuilegluseRgmihisileuLeu	480
Db		1381	GAAGAAGAGACATATGGGCAAGCACCTCATCTCATCGAAGCGACATCATACTGCTG	1440
Oy		481	HiscYbleuGlYlvsThrThr-----	487
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Oy		488	-----AsnHisgluhelieApArgIugiImetPhegluglAsnPyS	501
Db		1501	CGAACCTTCACCATCAGAACCCAGATTATGATGAGAGATGTTGAGAGAAATCTGC	1560
Oy		502	MetcGuseSerMetGlnAsnTylrProserThirArgerProserLeuSerSerhisPro	521
Db		1561	ATGAGAGATTCATATGCAAGAACTACCAATCCACAGAAATCTCTTCACTTCAGACCCA	1620
Oy		522	GlyLeuthrThrThrCyseCysserArgArgserLysLysThrThrhisleuProAnsSer	541
Db		1621	GGCTCATCTACCACTGCTGCTCCCGTGGTAGAAGAACACACACTCCCAATCT	1680
Oy		542	AsnLeuProAlaThrArgLeuArgSerMetGlngluLeuSerThrIleHisilglnGly	561
Db		1681	AACCTGCAGATACTCCGCTCGCAGCATGAGAGAGCTCACAGCATCATCATCCAGAGGC	1740
Oy		562	SerGluGlnPProserLeuThrThrserarSerSerLeuAsnLeuYalAspAspLy	581
Db		1741	AGTAGAGAGCCCTCCCTCTCAACACAGTGGCTCCAGCTTAATTGAAAGCAGACGCGGA	1800
Oy		582	LeuArgProAnsCyLysThrSerGlnIleThrThralaileieserIleProThrPro	601
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Oy		602	ProAlaLeuThrProGluGlyGluSerArgProPropoAlaserProGlyProAnsThr	621
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VERSION			AF187964.1	GI:5007796
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			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE			1 (bases 1 to 184)	
AUTHORS			Dilks,D., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.	
TITLE			Cloning and expression of the human kv4.3 potassium channel	
JOURNAL			J. Neurophysiol. 81 (4), 1974-1977 (1999)	
MEDLINE			99218223	
PUBMED			10200233	
REFERENCE			2 (bases 1 to 1984)	
AUTHORS			Dilks,D.W., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.	
TITLE			Direct Submission	
JOURNAL			Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research, CN	
FEATURES			8000, Room 1119A, Princeton, NJ 08543-8000, USA	
			Location/Qualifiers	

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Oy		581	GlyLeuArProAnCySlyVThrSeGlnIleThrhAlalleSerIleProThr	600
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Oy		601	ProProAlaleuThrProGIugLIgLUserArProProProAlaserProGLYProasn	620
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Oy		621	ThraSnilleProSerIleThrSerAsnValIalyVaIservAlleu	636
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 REFERENCE 1 (bases 1 to 2104)  
 AUTHORS Brill, A.M. and Calmejs, T.P.  
 TITLE KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  
 JOURNAL Patent: WO 9842833-A 5 01-OCT-1998;  
 BRIL ANTOINE MICHEL ALAIN (FR) ; CALMEJS THIERRY PAUL GERARD (FR)  
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VERSION	AR204886.1	GI:21502326	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2104)		
TITLE	Brill,A,Michel,Alain., Calmels,T,Paul, Gerard.,		
JOURNAL	Favre,J.-F.,Simon,Pierre., Jayre,J.-L. and Rouanet,S.		
FEATURES	Kv potassium channel polypeptides and polynucleotides		
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	1..2104		

ORIGIN

**Alignment Scores:**

Pred. No.:	3,98e-214	Length:	2104
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Percent Similarity:	99.21%	Conservative:	1
Best Local Similarity:	99.06%	Mismatches:	5
Query Match:	98.95%	Indels:	0
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US-10-062-879-4 (1-636) X AR204886 (1-2104)

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases)
Ohya,S.; Tanaka,M., Oku,T., Asai,Y., Watanabe,M., Giles,W.R. and
Imazumi,Y.
Molecular cloning and tissue distribution of an alternatively
spliced variant of an A-type K+ channel alpha-subunit, Kv4.3 in the
rat
FEBS Lett. 420 (1), 47-53 (1997)

JOURNAL   FEBS Lett. 420 (1), 47-53 (1997)
MEDLINE   98111009
PUBMED    9450548
REFERENCE 2 (bases 1 to 1968)
AUTHORS   Imazumi,Y.
TITLE      Direct Submission
JOURNAL    Submitted (06-MAY-1997) Yuji Imazumi, Nagoya City University,
Pharmacology and Therapeutics, 3-1 Tanabe-dori, Mizuho-ku, Nagoya,
Aichi 467, Japan (E-mail:yimaizumi@phar.nagoya-cu.ac.jp,
Tel:052-836-3433, Fax:052-836-3432)
LOCATION    Onalifilers

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ORIGIN
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Query Match: 98.93% Indels: 19
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US-10-062-879-4 (1-636) x AB003587 (1-1968)

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 VERSION AF048713.1 GI:2935435  
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 REFERENCE  
 AUTHORS Kong, W. and Tomaselli, G.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-FEB-1998) Medicine, Johns Hopkins University School of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA  
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 TITLE  
 1 (bases 1 to 2722)  
 Isbrandt,D., Leichter,T., Waldechütz,R., Zhu,X., Lühmann,U.,  
 Michel,U., Sauter,K. and Pongs,O.  
 Gene structures and expression profiles of three human KCND (Kv4)  
 potassium channels mediating A-type currents I(TO) and I(Sa)  
 Genomics 64 (2), 144-154 (2000)  
 JOURNAL  
 MEDLINE  
 20195625  
 PUBMED  
 10729221  
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 Zhu,X.R., Waldechütz,R., Isbrandt,D., Sauter,K. and Pongs,O.  
 Direct Submission  
 Submitted (15-JUN-1999) ZMNH, Institut fuer Neuzale  
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Best Local Similarity: 96.79% Mismatches: 2  
Query Match: 98.90% Indels: 19  
DB: 9 Gaps: 1

US-10-062-879-4 (1-636) x APL20491 (1-2722)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: April 13, 2005, 10:02:32 ; Search time 742.411 Seconds  
(without alignments)  
5071.258 Million cell updates/sec

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	3291.5	99.1	1968	12	ADP91397 Human Kv4
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16	2518	75.8	5333	12	ADM43514 Human ova
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18	2132.5	64.2	2711	4	AAH21246 Human Kv4
19	2123.5	64.0	3424	2	AAZ11901 Human pot
20	2090	63.0	2578	4	AAH99538 Human pro
21	1955	58.9	1716	4	ABL29811 Drosophila
22	1770	53.3	1737	12	ADP91396 Worm Kv4
23	1704	51.3	8075	4	ABL29810 Drosophila
24	1658.5	50.0	5404	11	ADM10924 Human O64
25	1658.5	50.0	5404	12	ADJ11254 Human ova
26	1658.5	50.0	5404	12	ADM43515 Human ova
27	1496.5	45.1	2033	4	AAH21248 Human KCN
28	1490.5	44.9	1121	12	ACH91582 Human gen
29	899	27.1	1083	4	AAH21264 Human Kv4
30	887	26.7	1597	11	ADM10925 Human O64
31	887	26.7	1597	12	ADJ11255 Human ova
32	887	26.7	1597	12	ADM43516 Human ova
33	863.5	26.0	3254	11	ADM10920 Human O64
34	863.5	26.0	3254	12	ADJ11250 Human ova
35	863.5	26.0	3254	12	ADM43511 Human ova
36	856	25.8	612	4	AAI28128 Human fce
37	856	25.8	612	4	ABA76453 Human fce
38	856	25.8	612	4	AAI57133 Probe #25
39	856	25.8	612	4	ABA40984 Probe #19
40	856	25.8	612	4	AAK51097 Human bon
41	856	25.8	612	4	AAK25090 Human bira
42	856	25.8	612	4	ABSS0654 Human liv
43	856	25.8	612	6	ABS24615 Human gen
44	758	22.8	3777	8	ABZ24713 Human pot
45	757.5	22.8	3339	4	ABL01915 Drosophila

## ALIGNMENTS

RESULT 1	ABN84401	standard; cDNA; 2064 BP.
XX	ABN84401;	
AC	01-OCT-2002	(first entry)
XX		
DT	Human Kv4.3 potassium channel (short form) cDNA.	
XX		
DE	Kv4.3: potassium channel; human; Alzheimer's disease; heart disease;	
XX	KM	neurotropic; neuroprotective; cardiac; gene therapy; gene; ss.
XX	XX	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	73..1983
FT		/*tag= a
FT		/product= "Kv4.3"
XX		
XX	US6395477-B1.	
XX		
XX	28-MAY-2002.	
XX		
PF	23-OCT-1998;	98US-00178109.
XX		
PR	23-OCT-1998;	98US-00178109.
XX		
PA	(AMHP ) AMERICAN HOME PROD CORP.	



XX Cockett MI, Dilks DW, Ling HC, Sokol PF,  
 XX WPI, 2002-556093/59.  
 DR P-PSDB, ABB79585.  
 XX  
 PT New isolated polynucleotide encoding human Kv4.3 potassium channel  
 PT polypeptide, useful as probe in a diagnostic method for detecting nucleic  
 PT acid encoding human Kv4.3, and for treating Alzheimer's and heart  
 PT diseases.  
 XX  
 PS Claim 7; Col 21-22; 19pp; English.  
 XX

CC The present sequence is that of cDNA encoding the short isoform of novel  
 CC human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been  
 CC identified. One form is full-length (hkV4.3 long) while the second form  
 CC has a deletion of 19 amino acids in the carboxy domain after the  
 CC predicted sixth transmembrane domain (hkV4.3 short). Human heart  
 CC primarily expresses hkV4.3 long, whereas human brain contains both forms.  
 CC To obtain the present hkV4.3 short cDNA, PCR amplification was performed  
 CC using primers that flanked the 57 bp insert in hkV4.3 long. The invention  
 CC provides Kv4.3 polypeptides, polynucleotides, and methods for producing  
 CC these polynucleotides. The Kv4.3 polypeptides and polynucleotides are  
 CC useful in the diagnosis, treatment and screening of human diseases  
 CC relating to an excess or deficiency of hkV4.3 activity, including  
 CC Alzheimer's disease and heart disease  
 XX  
 XX Sequence 2064 BP; 446 A; 678 C; 545 G; 395 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,476-273 Length: 2064  
 Score: 3320.00 Matches: 636  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Gaps: 0  
 DB: 6

US-10-062-879-4 (1-636) x ABN84401 (1-2064)

QY 1 MetAlaAlaGlyValAlaAlaATPLeuProPheAlaArgAlaAlaAlaIleGlyTyrPmet 20  
 Db 73 ATGCGCGCGGAGTTGGCGCTGCTGCTTTGGCGGCGCTGCGGCATCGGCTGAGATG 132  
 QY 21 ProValAlaAsnGlySerPmetProLeuAlaProAlaAspGlyAsnGlyAsnGlu 40  
 Db 133 CCGGTGGCCAACTGCCCCATGCCCCGCGCCGCAAGAAAGCGGAGATGAG 192  
 QY 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrTyrArgThrThrLeuGluArg 60  
 Db 193 CTGATTCTCTCAACGATGATGGCGGAGGTTCCAGACCTGGAGACCAAGCTGGAGCGC 252  
 QY 61 TyrProAspThrLeuLeuGlySerThrGluGlyGluPhePheAsnGluAspThrLys 80  
 Db 253 TACCGGACACCCCTGCGGAGACGACGAGAAGAGATTCTTTCAACGAGACACCAAG 312  
 QY 81 GluTyrPhePheAspAspAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100  
 Db 313 GAGATCTTCTTCAACCGGAGACCCCGAGGTGTTCGCGCTGCTCAACTTACCCGACAG 372  
 QY 101 GlyLeuLeuIleSerTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
 Db 373 GGGAGCTGCACTACCGCGCTACGATGATCTCTGCTTACCAACGAGAGCTGGCTTTC 432  
 QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysArgTyrGluGluTyrLysAspArgLys 140  
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 QY 141 ArgGluAsnAlaGluGluMetAspAspAspAspSerGluAsnGlnGlnGlnMet 160  
 Db 493 AGGAGAGAACCGCGGCTCATGAGACACGACGACGAGAAACCAAGAGATCCATG 552  
 QY 161 ProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThrSerThr 180

Db 553 CCTGCTCAGCTTCCGCGACAGACCATGAGCGGCGCTTCCAGAAACCCCAACAGCAGC 612  
 QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
 Db 613 CTGGCCCTGGCTCTTCTTACTAGTGAAGCTGCTTCTTCACTGCTGCTGCTATCAAC 672  
 QY 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220  
 Db 673 GTGGTGGAGACGGTCCGTGGGACCGGTCCCGGAGCAAGAGAGCTGCGTGGGGAG 732  
 QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
 Db 733 CGTACTCGTGGCTTCTTCTGCTGGACAGCGGCGGTGCGCATGATCTTACCGTGGAG 792  
 QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleAspSerValMetSer 260  
 Db 793 TACCTCCGCGCTTCTTCCGCGCTCCAGCGCTTCAACCGCTTCAACCGCTGATAGC 852  
 QY 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
 Db 853 ATCATGAGAGTGGTGGCATATGCTTACTTACATCGTCTGCTCATGACCAACAGAG 912  
 QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
 Db 913 GACGATCCCGGCGCTTGTGACGCTCCGCGCTTCCGCGCTTCCAGATCTTCAAGTTT 972  
 QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320  
 Db 973 TCCCGCCACTCCAGGGGCTGCGATCTGGGCTTACACATGAGAGAGCTGCTCCGAA 1032  
 QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
 Db 1033 CTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092  
 QY 341 TyrAlaGluGlySerSerSerAlaSerLysPheThrSerIleProAlaSerPheTyrTyr 360  
 Db 1093 TATGCCAGAAAGGGGCTCTGCGGAGAGTTCAAGATCCTGCTGCTTGTGATAC 1152  
 QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGly 380  
 Db 1153 ACCATTTTCAACATGACACACCTGGATACCGAGATCGGCTTAAAGACATGTCAGGG 1212  
 QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
 Db 1213 AAGATCTTCCGCTCATTTGCTTCTTGAAGTGGCTCTGCTGATTTGCCCTGCACTCCT 1272  
 QY 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
 Db 1273 GTGATTTTCAACTTAAAGCGGATTTTACCAACAGATCAAGAGCTGATTAACGCAAG 1332  
 QY 421 AlaGlnLysValAlaArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
 Db 1333 GCACAAAGAAAGGCGCGCTTGGCAGAGATCCGTGTGGCCAAAGACAGTTCAAATGCA 1392  
 QY 441 TyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThrGlyThrPro 460  
 Db 1393 TACCTGCAACAGAGCGGAGCGGCTCTTCAACAGAGGCGTGGAGCTGAGAGGACCCCA 1452  
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 Db 1453 GAAAGAGGACATGGGGAACACACCTCATTCAGAGGACCAAGCATCATCCTGCTG 1512  
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 Db 1513 CACTGCTGGAAAAAACAACATCAACAGAGTTTATGATGAGCAGATGTTTGACACAAAC 1572  
 QY 501 CysMetGluSerSerMetGluAsnTyrProSerThrArgSerProSerLeuSerSerHis 520  
 Db 1573 TGCATGGAGAGTTCAATCAACATCAACATCAACAGAGTCCCTCACTGTCAGCAGCAC 1632  
 QY 521 ProGlyLeuThrThrThrCysCysSerArgSerLysLysThrThrHisLeuProAsn 540  
 Db 1633 CAAAGCTCTCACTACCACTGCTGCTCCGCTGTTGTAAGAAAGACACACACCTGCCAAT 1692



QY 281 AspvAlSerGIyAlaPheValThrLeuArgValPheArgIlePheIysPhe 300  
 DB 841 GAGGTGCGCGCCCTTCGACAGCTCCGGCTTCGGGTTCAGATCTTCAGATT 900  
 QY 301 SerArgHisSerGIyLeuArgIleLeuGIyTyrThrLeuIysSerCysAlaSerGIu 320  
 DB 901 TCCGGCCATCCCAAGGCGCTCGCGATCTCGGCTTACACATAGAGAGCTGTGCTCCGA 960  
 QY 321 LeuGIyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThrValMetPhe 340  
 DB 961 CTGGGCTTCTCTCTCTCTCTCCCTCACCAATGGCCATCATCTTTGCCACTGATGTTT 1020  
 QY 341 TyrAlaGIuIySerGIySerAlaSerIyPheThrSerIleProAlaSerPheTyr 360  
 DB 1021 TATGCCAGAAAGGCTCTCTCGCAGCAAGTTACAGAGATCTCTGCTTGTGGTAC 1080  
 QY 361 ThrIleValThrMetThrThrLeuGIyTyrGIyAspMetValProIyThrIleArgIy 380  
 DB 1081 ACCATTGTCCATTCACATGACACATGGATACGAGACATGCTGCTTAAGACATTCAGAG 1140  
 QY 381 LysIlePheGIySerIleCysSerLeuSerGIyValLeuValIleAlaLeuProValPro 400  
 DB 1141 AAGATCTTCGGCTTCATCTCTCTCTGAGTGCGTCTGGTCAATGCTCCCTGCAAGTCCCT 1200  
 QY 401 ValIleValSerIyPheSerArgIleTyrHisGIyAsnGIyAlaArgIyAlaArgIy 420  
 DB 1201 GTATGTGTTCACATTTAGCCGATTTACACCAAGATCAGAGACTATTAACCGCAGG 1260  
 QY 421 AlaGIuIySerIyAlaArgIleAlaArgIleArgValAlaIyThrGIySerSerAlaAla 440  
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 QY 441 TyrLeuHisSerIySerIyArgIyLeuLeuAsnGIyAlaLeuGIuLeuThrGIyThrPro 460  
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 QY 461 GIuGIuIyHisMetGIyIyThrThrSerIleIleGIuSerIyHisIleIleLeu 480  
 DB 1381 GAAGAGAGACATGGGCAAGACCACTCATCATGAGGACATCATCACTGCTG 1440  
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 DB 1441 CACTGCTGAAAAAACCACTAACAGATTTATGATAGCAAGATTTTGAGCAAGAAC 1500  
 QY 501 CysMetGIuSerSerMetGIyAsnTyrProSerThrArgSerProSerLeuSerSerHis 520  
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 DB 1621 TCTAACCTGCAAGTACTCCGCTCGCAGCATGCAAGAGTTCAGCAGATCCATCCAG 1680  
 QY 561 GIySerGIuIyProSerLeuThrThrSerArgSerSerLeuAsnLeuIyAlaAsp 580  
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 QY 581 GIyLeuArgProAsnCysIyThrSerGIuIleThrThrAlaIleSerIleProThr 600  
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 QY 601 ProProAlaLeuThrProGIuGIyIyLeuSerArgProProAlaSerProGIyProAsn 620  
 DB 1801 CCCCAGCGCTAACCCAGAGGGGAAAGTGGCCACCCCTCGCAGGCCAGGCCCAAC 1860  
 QY 621 ThrAsnIleProSerIleThrSerAsnValIyIyValSerValIleu 636  
 DB 1861 ACGAACATCTCTTCATAGCCAGCAATGTTGTCAAGTCTCCGCTTG 1908  
 RESULT 3

ABN84400  
 ID ABN84400 standard; cDNA; 2121 BP.  
 AC ABN84400;  
 DT 01-OCT-2002 (first entry)  
 DE Human Kv4.3 potassium channel (long form) cDNA.  
 KW Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 73..2040  
 FT /\*tag= a  
 FT /\*product= "Kv4.3"  
 PN US6395477-B1:  
 PD 28-MAY-2002.  
 PF 23-OCT-1998; 98US-00178109.  
 PR 23-OCT-1998; 98US-00178109.  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 PI Cockett MI, Dilks DW, Ling HC, Sokol PT;  
 DR WPT; 2002-556093/59.  
 DR P-PSDB; ABB79584.  
 PT New isolated polynucleotide encoding human Kv4.3 potassium channel  
 PT polypeptide, useful as probe in a diagnostic method for detecting nucleic  
 PT acid encoding human Kv4.3, and for treating Alzheimer's and heart  
 PS diseases.  
 PS Claim 5; Col 15-18; 19pp; English.  
 CC The present sequence is that of cDNA encoding the long isoform of novel  
 CC human potassium channel Kv4.3. To obtain the cDNA, oligonucleotides based  
 CC on the published rat sequence were used to screen a whole heart cDNA  
 CC library. A 511 bp fragment was obtained and used as a probe to rescreen  
 CC the library. The resulting clones lacked the extreme 5' and 3' coding  
 CC regions, and 5' and 3' RACE was therefore used to amplify these sequences  
 CC from a human brainstem cDNA library. 2 isoforms of human Kv4.3 were  
 CC identified. One form is full-length (hkV4.3 long) while the second form  
 CC has a deletion of 15 amino acids in the carboxy domain after the  
 CC predicted sixth transmembrane domain (hkV4.3 short). Human heart  
 CC primarily expresses hkV4.3 long, whereas human brain contains both forms.  
 CC The invention provides Kv4.3 polypeptides, polynucleotides, and methods  
 CC for producing these polynucleotides. The Kv4.3 polypeptides and  
 CC polynucleotides are useful in the diagnosis, treatment and screening of  
 CC human diseases relating to an excess or deficiency of hkV4.3 activity,  
 CC including Alzheimer's disease and heart disease  
 XX  
 SQ Sequence 2121 BP; 457 A; 694 C; 557 G; 413 T; 0 U; 0 Other;  
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 Pred. No.: 1,67e-271 Length: 2121  
 Score: 3300.50 Matches: 636  
 Percent Similarity: 97.10% Conservative: 0  
 Best Local Similarity: 97.10% Mismatches: 0  
 Query Match: 99.41% Indels: 19  
 DB: 6 Gaps: 1  
 US-10-062-879-4 (1-636) x ABN84400 (1-2121)  
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 DB 73 ATGGCGCGCGAGTGTGCGGCTGCTTGTGCTCCGAGGCTGCGGCATCGGATGATG 132

QY 21 ProValAlaAsnCySPromerProLeuAlaProAlaAspLysAsnLysArgGlnAspGlu 40  
 Db 133 CCGGGGGCAATGGCCCATGGCCCTTGGCCCGGGCCGACAAAGAACAAAGCGAGATAG 192  
 QY 41 LeuIleValLeuAsnValSerGlyArgPheGlnThrTrpArgThrThreugluArg 60  
 Db 193 CTGATTGCTCTCAACGTAGTGGCGAGGTTCCAGACTGGAGGACCAAGCTGGAGCGC 252  
 QY 61 TyrProAspThrLeuGlySerThrGluysGluPhePheAsnGlnAspThrLys 80  
 Db 253 TACCCGGACACCTGCTGGAGCAACGAGAGAGGTTCTTCAACGAGACACCAAG 312  
 QY 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100  
 Db 313 GAGTACTTCTTCGACCGGGGACCCCGAGGTTCCTCCGCTCGTCTCACTTCCAGCGACG 372  
 QY 101 GlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
 Db 373 GGAAGAGTCACTACCGCGCTACGAGTGCATCTTGCTACGACGAGCGAGCTGCTTC 432  
 QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysGlyTyrGluGluTyrLysAspArgLys 140  
 Db 433 TACGGCATCTCCCGAGATCATCGGGGACTGCTGCTACGAGAGTACAGAGCGAG 492  
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 Db 493 AGGAGAAAGCCGAGCGGCTCATGGACAAACAACTGGAGAACACAGAGTCCATG 552  
 QY 161 ProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThrSerThr 180  
 Db 553 CCTCGCTCAGCTTCGCGACAGCATGtGGGGGCTTCGAGAACCCCAACCGACGACG 612  
 QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
 Db 613 CTGGCCCTGCTCTTACTACGTGACTGCTCTTCTTCATCGCTGCTCGCTCAACCAAC 672  
 QY 201 ValValGluThrValProCysGlyTyrValProGlySerLysGluLeuProCysGlyGlu 220  
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 QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
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 QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
 Db 793 TACCTCGTGGGCTTCTTGCGGCTCCAGCGCTACCGCTTCATCGGACGCTCATGAGC 852  
 QY 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
 Db 853 ATCATCGACGTGGTGGCATATGCCCTACTACATCGGTGGTATATCAACAAACAGAG 912  
 QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
 Db 913 GACGTGCTGGGCGCTTCTGTCAGCGTCCGGGTCTTCCGCTTCAAGATCTTCAAGTTT 972  
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 Db 1093 TATGGCGAAGAGGGTCTCTCGCGCAGAGTTCAACAACATCCCGCTCGTTTGGTAC 1152  
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 Db 1153 ACGATTGTACCATGACACACTGGGATACGAGACATGTGGCTTAAAGCATGTCCAGGG 1212

QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
 Db 1213 AAGATCTTGGCTCATCTGCTCTTGAAGTGGCGTCCGTGCTCATTTGCCCTTCCAGTCCCT 1272  
 QY 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
 Db 1273 GTGATTGTTTCAACTTTAAGCCGAGATTTTACCAACAGATTCAGAGCTGATTAACGACGG 1332  
 QY 421 AlaglnLysValArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
 Db 1333 GCACAAAGAAAGGCCCGCTTGCAGAGATCCGTGTGGCCAAACAGAGCATTCAGATTCGA 1392  
 QY 441 TyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThrGlyThrPro 460  
 Db 1393 TACCTGCACACAGACCGGCAAGCGGCTCTTCAACAGAGGGCTGAGAGTCAAGGCGACCCCA 1452  
 QY 461 GluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHisIleLeuLeu 480  
 Db 1453 GAAAGAGGACATAGGGGACAAACCACTCATTCAGAGCCAGCATCATCCTGCTG 1512  
 QY 481 HisCysLeuGluLysThrThr----- 487  
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 QY 488 -----AsnHisGluPheIleAspGluGlnMetPheGluGlnAsnCys 501  
 Db 1573 CGAAGCTCCACCATCAAGAACACAGAGTTTATGATGAGCAGATGTTGACACAGACTGC 1632  
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 Db 1633 ATGAGAGATTCAATGACAGAACTACCAATCCAAAGAGTCCCTCATCTGTCCAGCACCCA 1692  
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 Db 1693 GAGCTCATACCTAGCTGCTGCTCCGTCGTGTAAGTAAGAACACACACTCCCAATCT 1752  
 QY 542 AsnLeuProAlaThrArgLeuArgSerMetGlnLysLeuSerThrIleHisIleGlnGly 561  
 Db 1753 AACCTGCAGCTATCTGCTGCGCAGCATGCAAGAGCTCAGACAGATCCATCAGAGGC 1812  
 QY 562 SerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAspAspGly 581  
 Db 1813 AGTAGAGCAAGCCCTCCCTCACAACAGATCGCTCCAGCTTAAATTGAAAGAGAGACGGA 1872  
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 Db 1933 CCAAGCGTAAACCCAGAGGGGAAAGTGGCCACCCCTGCAAGCCAGAGGCCCAACAGC 1992  
 QY 622 AsnIleProSerIleThrSerAsnValValLysValSerValLeu 636  
 Db 1993 AACATTCCTTCATTAACAGCAATGTTGTCAAGTCTCTGCTTG 2037  
 RESULT 4  
 ADF91397  
 ID ADF91397 standard; cDNA; 1968 BP.  
 AC ADF91397;  
 XX 26-FEB-2004 (first entry)  
 DE Wild-type hXv4.3 cDNA #SEQ ID 4.  
 XX Antiarrhythmic; cardiovascular; anticonvulsant; cerebroprotective;  
 KW tranquilliser; sedative; neuroprotective; nootropic; antiparkinsonian;  
 KW nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist;  
 KW blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;  
 KW tachycardia; congestive heart failure; epilepsy; stroke;  
 KW traumatic brain injury; anxiety; insomnia; Alzheimer's disease;  
 KW Parkinson's disease; gene; ss.

XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX FT 1..1968  
 XX CDS /\*tag= a  
 FT /product= "hkv4.3"  
 XX  
 XX W02003097682-A1.  
 XX  
 XX 27-NOV-2003.  
 XX  
 XX 14-MAY-2003; 2003MO-IB002453.  
 XX  
 XX 15-MAY-2002; 2002GB-00011123.  
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 XX 15-MAY-2002; 2002US-0378076P.  
 XX  
 XX 15-MAY-2002; 2002US-0378131P.  
 XX  
 XX (DEVG-) DEVGEN NV.  
 XX  
 XX Kaletta TJ, Dewulf NE, Plaetinck GKM;  
 XX WPI; 2004-061981/06.  
 XX  
 XX P-PSDB; ADF91398.  
 XX  
 XX  
 XX New nematode worm expressing a heterologous nucleotide sequence encoding  
 XX a functional voltage-gated potassium channel of the Kv4 family, useful  
 XX for determining compounds that interact with the voltage-gated potassium  
 XX channel.  
 XX  
 XX Example 1; SEQ ID NO 4; 82pp; English.  
 XX  
 XX The invention relates to a nematode worm that expresses a heterologous  
 XX nucleotide sequence encoding a functional voltage-gated potassium channel  
 XX of the Kv4 family, or its analog, mutant, variant, homolog, ortholog,  
 XX part or fragment. The nematode worm is useful in determining whether a  
 XX compound interacts with the voltage-gated potassium channel of the Kv4  
 XX family or whether a compound is an agonist, antagonist, opener and/or  
 XX blocker of the voltage-gated potassium channel expressed by the nematode  
 XX worm. The methods are used for identifying and developing compounds that  
 XX interact with voltage-gated potassium channels of the Kv4 family. The  
 XX compositions may be used in the development and/or preparation of  
 XX compositions for pharmaceutical, agrochemical and/or veterinary use.  
 XX These may be used in preparing compositions for preventing or treating  
 XX diseases or conditions such as arrhythmia, tachycardia, congestive heart  
 XX failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia,  
 XX Alzheimer's disease or Parkinson's disease. The current sequence  
 XX represents wild-type hkv4.3 cDNA.  
 XX  
 XX Sequence 1968 BP; 426 A; 648 C; 511 G; 383 T; 0 U; 0 Other;  
 XX  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 8,79e-271 Length: 1968  
 XX Score: 3291.50 Matches: 634  
 XX Percent Similarity: 96.79% Conservative: 0  
 XX Best Local Similarity: 96.79% Mismatches: 2  
 XX Query Match: 99.14% Gaps: 19  
 XX DB: 12 Gaps: 1  
 XX  
 XX US-10-062-879-4 (1-636) x ADF91397 (1-1968)  
 XX  
 XX 1 MetAlaIaGlyAlaAlaATPLeuProPheAlaArgAlaAlaAlaIleGlyTTPMet 20  
 XX 1 ATGGCGCGCGAGTGGCGCTGGCTCTTTTGGCCGGGCTCGGCGCATCGGGTGGATG 60  
 XX  
 XX 21 ProValAlaAspCysPheMetProLeuAlaProAlaAspLysAsnLysArgLysArg 40  
 XX 61 CCGGTGGCCCAATGCCCATGCCCCCGCCGCAACAAGCAAGCGGCGAGATGAG 120  
 XX  
 XX 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGluArg 60  
 XX 121 CTGATTGCTCTCAACGATGAGTGGCGGAGGTTCCAGACTGGAGACCAAGCTGGAGCGC 180

QY 61 TyrProAspThrLeuLeuGlySerThrGluGlyGluPhePheAsnGluAspThrLys 80  
 Db 181 TACCCGACACCTGCTGGGCGACGACGAGAGGATTTCTTCAACAGAGACACCAAG 240  
 QY 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100  
 Db 241 GAGTACTTCTTGCACCGGAGCCCGAAGTGTTCGCGGTGCTCAACTTCAACCGCAGC 300  
 QY 101 GlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
 Db 301 GGGAAAGCTGCATCACCGCGCTACGAGTGCATCTCTCTCAACGACGAGCTGGCCCTTC 360  
 QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysGlySerTyrGluTyrLysAspArgLys 140  
 Db 361 TACGCACTCTCCCGAGATCATCGGAGACTGCTGTCAACAGAGATCAAGAGACCGCAG 420  
 QY 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnLysSerMet 160  
 Db 421 AGGAGAAACGCGGAGCGGCTCATGACGACACACTCGAGAACACACCGAGAGTCCATG 480  
 QY 161 ProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThrSerThr 180  
 Db 481 CCTCGCTCACTTCCGACAGACATGAGCGGCGCTTCCAGAACCCCAACACGACGACG 540  
 QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
 Db 541 CTGGCCCTGCTTCTTACTACGATGATGCTGCTTCACTGCTGCTGCTGCTATCAACAC 600  
 QY 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220  
 Db 601 GTGGTGGAGAGCGTGGCGGTGGTACGGTCCCGGCGCAAGAGAGCGCGGTGGGGAG 660  
 QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
 Db 661 CGCTACTGGTGGGCTTCTTCTGCTGGACACGCGCGCTGCATGATCTTCAACGCTGAG 720  
 QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleAspSerValMetSer 260  
 Db 721 TACTCTCGCGGCTTCTTCTGCGGCTCCAGCGGCTTCACTGCTGCTGCTGCTATACAGC 780  
 QY 261 IleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
 Db 781 ATCATCGACGCTGGTGGCATCATGCTTACTACATCGGTGCTGCTGCTGCTGCTGCTG 840  
 QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
 Db 841 GACGCTCGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320  
 Db 901 TCCCGCACCTCCAGGGGCTGCGGATCTGGGCTTACACACTGAAAGACTGCTGCTCCGAA 960  
 QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
 Db 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020  
 QY 341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTyrTyr 360  
 Db 1021 TATGCCGAGAAAGGCTCTCGGCGGCAAGTTCAACAGATCCTGCTGCTTGTGATAC 1080  
 QY 361 ThrIleValThrMetThrThrLeuGlyTyrArgLysPheValProLysThrIleAlaGly 380  
 Db 1081 ACCATTGTCAACATGACCACTGGATVACGGAACATGAGTCTTAAGACATTCGAGCGG 1140  
 QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
 Db 1141 AAGATCTTGGCTCATTTGCTCTTGAATGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
 QY 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
 Db 1201 GGATTTGTTTCAACTTATAGCGGATTTTACCAACGATCATGAGAGCTGATTAACGACG 1260  
 QY 421 AlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440

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Db 1261 GCACAAAAGAGCGCCGCTTGCAGATCCGTGTGGCCAAACAGGACGATTCAGATCA 1320
Qy 441 TyrluHhSerrLyArGAnGlyluenuenGuaIaLuGluLeuThrGlyThrPro 460
Db 1321 TACCTGCACACAGCGAGCGGCTCTCAACGAGGGCGCTGAGCTACGGGCCCCCA 1380
Qy 461 GluGluGluHhSmGlyLysThrThrsSerleuIleGluSerGlnHhHhIleuLeu 480
Db 1381 GAAGAGAGACATGGGCAACACCTCACTCATCGAGAGCCAGCATCATCCTGCTG 1440
Qy 481 HisCysLeuGluLysThrThrs----- 487
Db 1441 CACTGCCTGAGAAAACCACTGGGTGTCTATCTTGTGATGATCCCTGTATCTGTA 1500
Qy 488 -----AsnHhGluPheIleAspGluGlnMetPheGluGlnAsnGly 501
Db 1501 CGAACCTCCACCATCAAGAACCCAGAGTTATGTATGATGACAGATGTTGACAGAACTGC 1560
Qy 502 MetGluSerSerMetGlnAsnLysProSerThrArGSerProSerLeuSerSerHisPro 521
Db 1561 ATGAGAGTTCAATGCGAATCACTCCATCCACAGAACTCCCTCACTGCCAGCCCA 1620
Qy 522 GlyLeuThrThrThrsCysSerArGSerLysLysThrThrsIleuProAsnSer 541
Db 1621 GGCTCACTACCACTGCTGCTCCCGTGTAGTAAGAGAACACACCTGCCCAATTCT 1680
Qy 542 AsnLeuProAlaThrArGLeuArGSerMetGlnLysSerThrThrsIleGlnGly 561
Db 1681 AACCTGCACGCTACTCGCTCGACGACATGCAAGGCTCACACACATCCATCCAGGCG 1740
Qy 562 SerGluGlnProSerLeuThrThrsArGSerSerLeuAsnLeuValAspGly 581
Db 1741 AGTAGAGAGCCCTCCCTCAACAGCTGCTCAGCTTAATTGAAAGACAGACGCA 1800
Qy 582 LeuArGProAsnGlyThrSerGlnLysThrThrsAlaIleSerIleProThrPro 601
Db 1801 CTGAGACCAAACTGCAAAACATCCAGATCCACAGCATCATCAGATCCCACTGCC 1860
Qy 602 ProAlaLeuThrProGluGlyGluSerArGProProAlaSerProGlyProAsnThr 621
Db 1861 CCACGCGCTAAACCCAGAGGGGAAAGTGGCCACCCCTGCGAGGCCGCCCAACG 1920
Qy 622 AsnIleProSerIleThrSerAsnValValysValSerValLeu 636
Db 1921 AACATCTCTTCATAGCCAGCAATGTGTCAAGGTCTCCGCTTG 1965

RESULT 5
ID AAV61572 standard; cDNA; 2072 BP.
XX
AC AAV61572;
DT 11-JAN-1999 (first entry)
XX
DE Human Kv potassium channel hKv4.3 (longer isoform) cDNA.
KW Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;
KW therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key 1.1965 Location/Qualifiers
FT CDS /*tag= a
XX
XX MO9842833-A2.
XX
PD 01-OCT-1998.
XX
PF 23-MAR-1998; 98WO-EP001901.
XX
PR 27-MAR-1997; 97GB-00006377.
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PR 09-DEC-1997; 97EP-00402971.
PR 11-DEC-1997; 97EP-00403007.
XX
PA (SMIK ) SMITHKLINE BEECHAM LAB PHARM.
PI Bril AMA, Calmels TPG, Faivre JSP, Javre J, Rouanet S;
DR WPI; 1998-542277/46.
P-PSDB; AAW79590.
XX
PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding
PT polynucleotide(s) useful in the treatment of disorders including cardiac
PT arrhythmias and Alzheimer's disease.
XX
PS Claim 2; Page 26; 47pp; English.
XX
CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see
CC AAW79590). It shows about 92% identity in 1932 nucleotides to rat Kv4.3.
CC A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated
CC from human heart cDNA by PCR amplification (see AAV61574-77). Another
CC claimed polynucleotide (see AAV61571) encodes an isoform (see AAW79589)
CC of hKv4.3 having 19 fewer amino acid residues. The invention relates to
CC these hKv4.3 polynucleotides and polypeptides and to methods for
CC producing such polypeptides by recombinant techniques. Also claimed are
CC methods for utilising the hKv4.3 polynucleotides for the treatment of
CC subjects in need of enhanced or reduced activity or expression of hKv4.3
CC polypeptide. These include the treatment of cardiac arrhythmias and
CC Alzheimer's disease. The invention can also be used to identify agonists
CC and antagonists of hKv4.3, and to detect disease associated with
CC inappropriate hKv4.3 expression or activity
XX
SQ Sequence 2072 BP; 449 A; 681 C; 541 G; 401 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 9.47e-271 Length: 2072
Score: 3291.50 Matches: 634
Percent Similarity: 96.79% Conservative: 0
Best Local Similarity: 96.79% Mismatches: 2
Query Match: 99.14% Indels: 19
DB: Gaps: 1
US-10-062-879-4 (1-636) x AAV61572 (1-2072)
Qy 1 MetAlaIaGlyValAlaAlaTProLeuProPheAlaArGAlaIaIaIleGlyTrpMet 20
Db 1 ATGGCGGAGAGAGTTGCAAGCTGCTGCTTTTCCCGGGCTGGCCATGGGGTGAAG 60
Qy 21 ProValAlaAsnGlyProMetProLeuAlaProAlaAspLysAsnLysArGAlaAspGlu 40
Db 61 CCGGTGGCAAACTGCCCATGCCCCCTG6CCCGGCGCAAGAACAGCGGACAGATGAG 120
Qy 41 LeuIleValLeuAsnValSerGlyArGArGheGlnThrThrsPheGlnThrLeuGluArg 60
Db 121 CTGATTGTCTTCAACGTGAGTGGCGGAGGTTCCAGACTGAGAGACCACTGAGAGGC 180
Qy 61 TyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThrLys 80
Db 181 TACCGGACACCTGCTGGGAGCAAGAGAGAGTTCTTCTTCAACGAGAGACCAAG 240
Qy 81 GluTyrPhePheAspArGAspProGluValPheArGValLeuAsnPheTyrArgThr 100
Db 241 GAGTACTTCTTTCGACCGGAGACCCGAGGTGTCGCGTGGCGTCACTTACCGGACG 300
Qy 101 GlyLysLeuHhIleTyrProArGTYrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120
Db 301 GGGAAAGCTGCACTACCGCGCTACGAGTGCATCTCTCTTACGACGAGAGCTGGCTTC 360
Qy 121 TyrGlyIleLeuProGluIleIleGlyAspCysArGTYrGluGluTyrLysAspArgLys 140
Db 361 TACGGCATCTCTCCGAGATCATGGGAGCTGCTGCTACAGAGATCAAGACCGGACAG 420
Qy 141 ArgGluAsnAlaGluArGLeuMetAspAspAsnAspSerGluAsnGlnGluSerMet 160
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Db 421 AGGGAGAACGCCGCGCTCATGGACAGACGACTCGGAGAACACGAGTCCATG 480  
 Qy 161 ProSerLeuSerPheArgIleThrMetTyrAlaAlaPheGluAsnProHisThrSerThr 180  
 Db 481 CCCCTCGCTCAGCTTCCCGCCAGACCATGTGGCGGCTTCGAGAACCCCGCCACACGACG 540  
 Qy 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
 Db 541 CTGGCCCTGGTCTTCTACAGTACGTGGCTCTTCACTGCTGTCTGGATCAGACCAAC 600  
 Qy 201 ValValGluThrValProCysGlyThrValProGlySerIleGluLeuProCysGlyGlu 220  
 Db 601 GTGGTGAAGACGGTGGCGGTGGGACGGTCCCGGGAGCAAGAGGCGTCCGGGGAG 660  
 Qy 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
 Db 661 CGTACTCGGTGGGCTTCTTCTGCTGACACGGCGGTGCTCATGATCTTCAACGGGAG 720  
 Qy 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
 Db 721 TACTCTCGCGGCTCTTCGCGGCTCCAGCGGCTTCACTGACCGACCGTCAATGAGC 780  
 Qy 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
 Db 781 ATCATGACGTGGTGGGCTCATCATGCTCTTACTCATGCTGTGTCATGACCAACAGAG 840  
 Qy 281 AspValSerGlyValaPheValThrLeuArgValPheArgValPheArgIlePheIlePhe 300  
 Db 841 GACGTGTCCGGCGCTTCGTACACGCTCCGGGCTCTCCGCTCTTCAGGATCTTCAAGTTT 900  
 Qy 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrThrLeuLeuSerCysAlaSerGlu 320  
 Db 901 TCCGCGCATCTCCAGGCGCTGCGGATCTGGCTGACACTGGAAGCTGTGCTCCGAG 960  
 Qy 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
 Db 961 CTGGGCTTTCTTCTCTTCTCCCTCAGCATGCGCATCATCTTTGGCATGTGATGTTT 1020  
 Qy 341 TyrAlaGluGlySerSerAlaSerLeuPheThrSerIleProAlaSerPheTyrPyr 360  
 Db 1021 TATGCCAGAAAGGCGCTCTCGGCGAGCAAGTTCACAAAGCATCCCTGCTGTGGTGTAC 1080  
 Qy 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIleThrIleAlaGly 380  
 Db 1081 ACCATTGTCAACATGACACACATGAGTACGAGACATGATGCTTAAGACATTTGAGAG 1140  
 Qy 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
 Db 1141 AAGATCTTCGGCTCATCTGCTCTTGAAGTGGCTCTGCTCATTTGCCCTGCCAGTCCCT 1200  
 Qy 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
 Db 1201 GTGATTTGTTTCACTTTAGCCGGAATTATACACAGAAATCAGAGAGCTGATTAACGAG 1260  
 Qy 421 AlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
 Db 1261 GCACAAAAGAGGCGCTTCCAGAGATCGGTGGCCAAAACAGGCACTTGAATGAC 1320  
 Qy 441 TyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThrGlyThrPro 460  
 Db 1321 TACTGTGACAGCAAGCCGACGCGCTCTTCAACAGAGCGCTGAGCTGAGCGGACCCCA 1380  
 Qy 461 GluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHisIleLeuLeu 480  
 Db 1381 GAAGAGAGGACATGAGGCAAGACCACTCATCTCAGAGAGCAGCATCATCACTGCTG 1440  
 Qy 481 HisGlyLeuGluLysThrThr----- 487  
 Db 1441 CACTGCTCGAAAACCACTGGGTGTCTATCTTGATGATATCCCTGTATCTGTA 1500  
 Qy 488 -----AsnHisGluPheIleAspGluGlnMetPheGluGlnAsnCys 501  
 Db 1501 CGAACCTTCACCATCAAGAACCAAGATTTATATGACAGATGTTTGACAGAACTGC 1560

Qy 502 MetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSerSerHisPro 521  
 Db 1561 ATGGAGATTTCAAGTACGAGAACTACCATCCACCAAGAAATCCCTCATCTGTCAGCCACCA 1620  
 Qy 522 GlyLeuThrThrThrCysCysSerArgSerLysThrThrHisLeuProAsnSer 541  
 Db 1621 GGCTCATCTACCATCTGCTGCTCCCGTGTAGTAAAGAACACACACCTGCCAATTCT 1680  
 Qy 542 AsnLeuProAlaThrArgLeuArgSerMetGlnLeuSerThrIleHisIleGlnGly 561  
 Db 1681 AACCTGCAGCTTACCTGCTGCTGCGACATGAGAGAGCTCAGACAGATCCACATCAGGCG 1740  
 Qy 562 SerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLysAlaAspArgGly 581  
 Db 1741 AGTGGAGCGCCCTCCCTCCACACAGTCTCCGCTTAATTTGAAGACAGACGAGGA 1800  
 Qy 582 LeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleSerIleProThrPro 601  
 Db 1801 CTGAGACCAACTGCAAAACATCCCAATCACACAGCATCATCAGCATCCCATCTCC 1860  
 Qy 602 ProAlaLeuThrProGluGlyGluSerArgProProProAlaSerProGlyProAsnThr 621  
 Db 1861 CCAGCGCTAACCCCAAGAGGGGAAAGTCGGCCACCCCTGCCAGCCAGGCCCCAACAGC 1920  
 Qy 622 AsnIleProSerIleThrSerAsnValValLysValSerValLeu 636  
 Db 1921 AACATTTCTTCATAGCCAGCAATGTGTCAAGGTCTCCGCTTG 1965  
 RESULT 6  
 AAV61573  
 ID AAV61573 standard; cDNA, 2104 BP.  
 AC AAV61573;  
 DT 11-JAN-1999 (first entry)  
 DE Human Kv potassium channel hKv4.3 cDNA.  
 KW Potassium channel; Kv; hKv4.3; human; Alzheimer's disease; arrhythmia;  
 KW therapy; diagnosis; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..1911  
 FT /\*tag= a  
 PN W09842833-A2.  
 XX  
 PD 01-OCT-1998.  
 XX  
 PF 23-MAR-1998; 98MO-EP001901.  
 XX  
 PR 27-MAR-1997; 97GB-00006377.  
 PR 09-DEC-1997; 97BP-00402971.  
 PR 11-DEC-1997; 97BP-00403007.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM LAB PHARM.  
 XX  
 PI Bril AMM, Calmels TPG, Faivre JSP, Javre J, Rouanet S;  
 XX  
 DR WPI; 1998-542277/46.  
 DR P-PSDB; AAW79591.  
 XX  
 PT New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding  
 PT polynucleotide(s) useful in the treatment of disorders including cardiac  
 PT arrhythmias and Alzheimer's disease.  
 XX  
 PS Claim 18; Page 27; 47pp; English.  
 CC This cDNA sequence codes for human Kv potassium channel hKv4.3 (see  
 CC AAW79591). It was isolated using expressed sequence tag analysis. The



CC sequence has about 91% identity in 1914 nucleotide residues with rat  
 CC Kv4.3 potassium channel. Full-length hKv4.3 cDNA clones (see AAV61571-72)  
 CC are also claimed. The invention relates to hKv4.3 polynucleotides and  
 CC polypeptides and to methods for producing such polypeptides by  
 CC recombinant techniques. Also claimed are methods for utilizing hKv4.3  
 CC polynucleotides for the treatment of subjects in need of enhanced or  
 CC reduced activity or expression of hKv4.3 polypeptide. These include the  
 CC treatment of cardiac arrhythmias and Alzheimer's disease. The invention  
 CC can also be used to identify agonists and antagonists of hKv4.3, and to  
 CC detect disease associated with inappropriate hKv4.3 expression or  
 CC activity

XX Sequence 2104 BP; 462 A; 679 C; 560 G; 403 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	3,48e-270	Length:	2104
Score:	3285.00	Matches:	630
Percent Similarity:	99.21%	Conservative:	1
Best Local Similarity:	99.06%	Mismatches:	5
Query Match:	98.95%	Indels:	0
DB:	2	Gaps:	0

US-10-062-879-4 (1-636) x AAV61573 (1-2104)

Qy 1 MetAlaAlaGlyValAlaAlaTPrLeuProPheAlaArgAlaAlaAlaIleGlyTPrMet 20  
 Db 1 ATGGCGGAGAGAGATTGACGCTGGCTGCTTTTGGCCGGGCTGGCCATCGGGTGGTGG 60  
 Qy 21 ProValAlaAsnCySPromerProLeuAlaProAlaAspIleAsnIleArgGlnAspGlu 40  
 Db 61 CCGGTGGCCAACTCCCATGCCCTGGCCCGCGCGCAAGAAACAAACGGCGAGATGAG 120  
 Qy 41 LeuIleValLeuAsnValSerGlyValArgArgPheGlnThrTPrArgPheThrLeuGlnArg 60  
 Db 121 CTGATTGTCTTCAACGAGAGGAGGAGGAGGTTCCAGACTGAGAGCAACCTGGAGGGC 180  
 Qy 61 TyrProAspThrLeuGlySerThrGluIleGluPhePheAsnGluAspThrIle 80  
 Db 181 TACCGGAGACCCCTGGCTGGGAGCAGCGAAGAGATTCTTCTTCAAGAGAGACCCAG 240  
 Qy 81 GluIlePhePheAspArgAspProGluValIleArgCysValIleAsnIlePheThr 100  
 Db 241 GAGTACTTCTTCCAGCCGGGAGCCCGAGGAGTTCGGCTCGTCACTTCTTACCGCAG 300  
 Qy 101 GlyIleLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
 Db 301 GGGAGAGCTGACATACAGCGCTACAGAGTCACTCTGCTTCAAGCAGAGACTGGCTTC 360  
 Qy 121 TyrGlyIleLeuProGluIleIleGlyValAspCysTyrGluGluTyrIleAspArgIle 140  
 Db 361 TACGGCATCTCTCCGGAGATCATCGGGAGCTGCTGCTTCAAGAGTCAAGAGCCGAG 420  
 Qy 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGluIleSerMet 160  
 Db 421 AGGAGAGACCGCGAGGCTCATGAGCAACAGCTCGAGAGAACCAAGAGTCCATG 480  
 Qy 161 ProSerLeuSerPheArgGlnThrMetTPrArgAlaPheGluAsnProIleThrSerThr 180  
 Db 481 CCCCTGGCTCAGCTTCCGACACCATGCGGGGCTTTCAGAAACCCCAACACACAGCAG 540  
 Qy 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
 Db 541 CTGGCCCTGGCTTCTTCTTCACTGAGCTGCTTCTTCTTCTGCTGCTGCTGCTGCTG 600  
 Qy 201 ValValGluThrValProCysGlyThrValProGlySerIleGluLeuProCysGlyGlu 220  
 Db 601 GTGGTGAAGACGGTGGCGGAGCAGGTCCTGGGAGCAAGAGAGCTGCGTGGGGAG 660  
 Qy 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
 Db 661 CGCTACTGAGTGGGCTTCTTCTTCTGCTGAGCAGGAGGTCGCTCATGATCTTACCGTGG 720  
 Qy 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260

Db 721 TACTCTCCGCGCTTCTGCGGCTCCAGCGCTTACCGCTTACCGGAGGTATGAGC 780  
 Qy 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
 Db 781 ATCATCGACGGTGGGCGCATATGCTACTTACTGCTGGTGCATATCAACACAGAG 840  
 Qy 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheIlePhe 300  
 Db 841 GACGTGTCCGGCGCTTGTGACGCTCCGGGCTTCCGGCTTCCAGATCTCCAAAGTTT 900  
 Qy 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuIleSerCysAlaSerGlu 320  
 Db 901 TCCGCGCACTCCAGGGGCTCGGATCTGGGCTTACACATGAGAGAGCTGGCTCCAA 960  
 Qy 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
 Db 961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020  
 Qy 341 TyrAlaGluIleGlySerSerAlaSerIlePheThrSerIleProAlaSerPheTPrIle 360  
 Db 1021 TATGCCAGAGAGGCTCTCTGCGCAGCAAGTTCACAGATCCCTGCTTGTGTATC 1080  
 Qy 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIleThrIleAlaGly 380  
 Db 1081 ACCATTGTCACTAGACCACTGGATACGAGACATGAGGCTTAAAGATTCAGAGAGG 1140  
 Qy 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
 Db 1141 AAGATCTTGGCTCATCTGCTCTTGAAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200  
 Qy 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspIleArgArg 420  
 Db 1201 GTGATTGTCTTCAACTTATAGCCGATTTTACCAACAGAAACAGAGCTGATTAACGCA 1260  
 Qy 421 AlaGlnIleIleValIleArgLeuAlaArgIleArgValAlaIleArgIleSerSerAsnAla 440  
 Db 1261 GCACAAAGAGAGGCGCGCTTCCAGAGATCGTGTGGCAAAACAGGAGTTCAGATGCA 1320  
 Qy 441 TyrLeuHisSerIleValGlnAsnGlyLeuLeuAsnGluAlaLeuGluLeuThrGlyThrPro 460  
 Db 1321 TACCTGACACAGCAAGCCCAACAGGCTCTTCAACAGAGCGCTGAGCTGACGGGAC 1380  
 Qy 461 GluGluGluHisMetGlyIleThrThrSerLeuIleGluSerGlnHisIleHisIleLeu 480  
 Db 1381 GAAAGAGAGCAGTGGGAGAGACCACTCATCTATCGAGCCGATCATCACTGCTG 1440  
 Qy 481 HisCysLeuGluIleThrThrAsnHisGluPheIleAspGluIleMetPheGluGlnAsn 500  
 Db 1441 CACTGCTGGAAAGAACCACTAACCAAGATTTATGATGAGAGATGTTGAGCAGAGAC 1500  
 Qy 501 CysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSerSerHis 520  
 Db 1501 TGCATGAGAGATTCAAGAGAACTACCACTCCCAAGAGTCCCTCATCTGTCCAGCCAC 1560  
 Qy 521 ProGlyLeuThrThrThrCysCysSerArgArgSerIleValThrThrHisIleuProAsn 540  
 Db 1561 CGAGGCTCTACTACACTGCTGCTCCGCTGATGATGAAGAGACACACACTGCGCAAT 1620  
 Qy 541 SerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIleHisIleGln 560  
 Db 1621 TCTAACCTGCAGCTTACTCGCTGCGCAGATGCAAGAGTCAACACAGATCATCATCAG 1680  
 Qy 561 GlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAspAsp 580  
 Db 1681 GGCAGTGAAGAGCCCTCTCTCAACACAGTCTCCAGCTTAAATTGAAGAGAGAGAC 1740  
 Qy 581 GlyLeuArgProAsnCysIleThrSerGlnIleThrThrAlaIleIleSerIleProThr 600  
 Db 1741 GGACTGAGACCAACTGCAAAACATCCCAAGTACCAAGCATCATCAGATCCCACT 1800  
 Qy 601 ProProAlaLeuThrProGluGlyIleIleArgProProAlaSerProGlyProAsn 620







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Db 730 ACTGGAGAGCTCACTATCTCCGACAGTGCATCTGCTTACATAGAAAGATCGGCC 789
Qy 120 PheTYrGly1LeuLeuProGluIleIleGlyASPcysCysEtyrGluGluTYrIlyAspArg 139
Db 790 TTCTTTGGCCTCATCCCGAATCATCGGCACTGCTGTTATGAGAGATACAAGATCGC 849
Qy 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSer 159
Db 850 AGCGAGAGAAACCCGACGCGCTGACGACGACGCGGATACCGACCGCTGGCGAGAC 909
Qy 160 ---MetProSerLeuSerPheArgGlnThMetTrpArgAlaPheGluAsnProHisThr 178
Db 910 GCCCTGCCACCACTGATCGAAGCAGAGGCTGTGAGGCGCTTCGAGAACCCCAACACC 969
Qy 179 SerTrpLeuAlaLeuValPheTYrTYrValThrGlyPhePheIleAlaValSerValIle 198
Db 970 AGCAGCATGCGCCCTGGGTCTTACTATGTCACGGGGTTTTTCTATCCGCTCTGTCTAC 1029
Qy 199 ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
Db 1030 GCCAATGCTGGTGAACAGTGCCTGGATCAAGCCCAAGTCACTTAAAGAACTGCCCC 1089
Qy 218 CysGlyGluArgTYrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db 1090 TGTGAGAGCGGATGCTGTGCGCTTCTGTGCTGACAGCGCTGTGCTGATGATCTTC 1149
Qy 238 ThrValGluTYrLeuLeuArgLeuPheAlaAlaProSerArgTYrArgPheIleArgSer 257
Db 1150 ACAGTTGAGTATTTGGCTTGGCTGGCGTGCAGCGCTTATGCTTACCGTTTGGCTAGT 1209
Qy 258 ValMetSerIleIleAspValAlaIleMetProTYrTYrIleGlyLeuValMetThr 277
Db 1210 GTATGTAGTATCATCGACGTTGGTGCATCTGCTTATTTACATTTGGCTGGTGAAGACA 1269
Qy 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
Db 1270 GACATATGAGACGTCACGAGGCGCTTGTGACATCGAGTCTTCGGGGCTTCAGAGATC 1329
Qy 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTYrThrLeuLysSerCys 317
Db 1330 TTTTAGATTTTCCGCCCACTCTCAAGGCTGCGCATCTGGGGATACACATGAAGATTTGT 1389
Qy 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThMetAlaIleIleIlePheAlaThr 337
Db 1390 GCCTCAGAAATTTGGGCTTCTGCTTTCTCCGTCACATGCTATTCATCTTCCTGTACA 1449
Qy 338 ValMetPheTYrAlaGluArgLysSerSerAlaSerLysPheThrSerIleProAlaSer 357
Db 1450 GTTATGTCTTACGACGAGAGAGGCTTCTGCTAGCAGATTCACACAGCATCTCTGACGCC 1509
Qy 358 PheTrpTYrThrIleValThrMetThrThrLeuGlyTYrGlyAspMetValProLysThr 377
Db 1510 TTCTGATATCATCTGTCACATGACACACATGAGGATGTGATGATGGCCAAAACCC 1569
Qy 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397
Db 1570 ATAGCAGGAGAAATTTTGGTCTTATCTGTTCTGCTGAGTGGGCTTGGTCAATGTGCTCA 1629
Qy 398 ProValProValIleValSerAsnPheSerArgIleTYrHisGlnAsnGlnAlaAsp 417
Db 1630 CTTGTTCCGGTGAATGATCACTTCACTGATGATCAACACAGATCAACAGACAGAC 1689
Qy 418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437
Db 1690 AAACGAGGCGCAAAAGAAAGCTAGCTGCGCAGATCCGGCAGCGCAAAACGAGAC 1749
Qy 438 SerAsnAlaTYrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457
Db 1750 GCAATATCTTACATGACAGCAAAACGGAATGTTTACTCATCATCAGCTGACAG---TCC 1806
Qy 458 GlyThrProGluGluGlnHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477

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Db 1807 TCAGAGATGACAGGCTTTGTTAGCAATCCGGCTCCAGCTTTGAACCCAGACAC 1866
Qy 478 HisLeuLeuHisCysLeuGluLysThrThrAsnHisGluPheIleAspGluGlnMetPhe 497
Db 1867 CACCTGCTTCACTCCCTCGAAGAAAAACCAAGATCAACAGTTTGTGAGCAAGAACTTTT 1926
Qy 498 GlnGlnAsnGlyMetGlnGluSerMetGlnAsnTYrProSerThrArgSerProSerLeu 517
Db 1927 GAAGAAAGCTGACAGAAAGTTGACACTGTATGCTCTTCAAGTCAAGTCTTCACTG 1986
Qy 518 SerSerHisProGlyLeuLeuThrThrCysCysSerArgArgSerLysLysThrHis 537
Db 1987 TCTTCAACACAGAGATGATCACCAGACCTGCTGTTCAAGACAGACAAACAACTTTCCG 2046
Qy 538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle 557
Db 2047 ATCCCAATGCAATGATATTCAGAAAGCCATCAAGTATGATACAAAGAACTCAGACGATT 2106
Qy 558 HisIleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLys 577
Db 2107 CAGATCAATGTGTGAGAGAAACCTCTGTCAACAGCGATCAAGTTTAAATGCCAA 2166
Qy 578 AlaAspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleIleSer 597
Db 2167 ATGGAAGAGTGTGTTAACTAACTGAACCAACTTATGATGACTACAGCAATATATAGC 2226
Qy 598 IleProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAla 615
Db 2227 ATCCCAACACCTCCAGTAACCAACACAGAGAGACATGAGCCAGATCCCTGAGTAC 2286
Qy 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerVal 635
Db 2287 TCAGAGAGA-----AAATGTGACAGATTTCTGCT 2316
Qy 636 Leu 636
Db 2317 TTG 2319

RESULT 9
ID ADJ11252
ADJ11252 standard, DNA, 2351 BP.
AC ADJ11252;
XX
XX 15-APR-2004 (first entry)
XX
XX
DE Human ovarian tumour antigen DNA SeqID 253.
XX
XX human; ds; ovarian cancer; immunogenic; antibody;
XX antigen presenting cell; APC; immune system cell; T cell; tumourigenic;
XX cytostatic; gene.
XX Homo sapiens.
XX
XX US2003222056-A1.
XX
XX 18-DEC-2003.
XX
XX 14-FEB-2003; 2003US-00369186.
XX
XX 10-SEP-1999; 98US-00394374.
XX 01-MAY-2000; 2000US-00561778.
XX 15-AUG-2000; 2000US-00640173.
XX 07-SEP-2000; 2000US-00656668.
XX 14-NOV-2000; 2000US-00713550.
XX 03-APR-2001; 2001US-00825294.
XX 02-OCT-2001; 2001US-00970966.
XX 02-AUG-2002; 2002US-00212677.
XX 05-FEB-2003; 2003US-00361811.
XX (CORI-) CORIXA CORP.
XX
XX Fanger GR, Fling SP;
PI

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Db      2047 ATCCCAATGCCAATGATATCAGAGACCATCAAGTATGATACAGAACTCAGCAGATT 2106
QY      558 Hs11gclnglysergluglnProSerLeuThrThrSerArgSerLeuAnuLeuYs 577
        |||:::|||||
Db      2107 CAGATCAGATGTGTGAGAGAAACACTGTGTCTTAAACAGCCGATCCAGTTTAAATGCCAA 2166
QY      578 AlaAspAspGlyLeuArgProAsnGlySerThrSerGlnLeuThrAlaIleIleSer 597
        :::::|||||
Db      2167 ATGGAAGAGTGTCTTAACTGTAACCTTATGTGACTACAGCAATATATMACC 2226
QY      598 IleProThrProProAlaLeuThrProGluGlyGlySerArgPro-----ProProAla 615
        |||:::|||||
Db      2227 ATCCCAACACTCTCAGTAACCAACAGAGAGAGATAGGCAATCCCTAGATAC 2286
QY      616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValIysValSerVal 635
        |||:::|||||
Db      2287 TCAGGAGGA-----AAATATGTCTCAGAGTTCTGTCT 2316
QY      636 Leu 636
        |||
Db      2317 TTG 2319

RESULT 10
ADM43513
ID      ADM43513 standard; DNA: 2351 BP.
XX      ADM43513;
AC      ADM43513;
DT      03-JUN-2004 (first entry)
XX      DE      Human ovarian cancer CDNA homologous DNA #7.
XX      KW      de; human; cancer; ovarian cancer; ovarian carcinoma; gene.
XX      OS      Homo sapiens.
XX      PN      US2003129192-A1.
XX      PD      10-JUL-2003.
XX      PF      02-AUG-2002; 2002US-00212677.
XX      PR      10-SEP-1999; 99US-00394374.
XX      PR      01-MAY-2000; 2000US-00561778.
XX      PR      15-AUG-2000; 2000US-00640173.
XX      PR      07-SEP-2000; 2000US-00656668.
XX      PR      14-NOV-2000; 2000US-00713550.
XX      PR      03-APR-2001; 2001US-00825294.
XX      PR      02-OCT-2001; 2001US-00970966..
XX      PA      (CORI-) CORIXA CORP.
XX      PI      Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;
XX      DR      WPI; 2004-051070/05.
XX      DR      P-PSDB; ADM43519.
XX      PT      New isolated polynucleotide encoding an ovarian tumor protein for use in
XX      PT      diagnosing, preventing or treating cancer, particularly ovarian cancer.
XX      PS      Claim 1; SEQ ID NO 253; 220bp; English.
XX      CC      The invention relates to an isolated polynucleotide. The invention is
XX      CC      used to diagnose, prevent or treat cancer, particularly ovarian cancer.
XX      CC      The present sequence represents a human ovarian carcinoma CDNA homologous
XX      CC      DNA.
SQ      Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,266-204 Length: 2351
Score: 2518.00 Matches: 486
Percent Similarity: 86.58% Conservative: 69

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Best Local Similarity: 75.82% Mismatches: 70
Query Match: 75.84% Index: 16
DB: 12 Gaps: 6
US-10-062-879-4 (1-636) x ADM43513 (1-2351)

QY      1 MetAlaIaGlyValAlaIaTProLeuProPheAlaArgAlaAlaIleGlyTProMet 20
        |||:::|||||
Db      430 ATGGCGGGGGGGGGGCGAGCGCTGCTCTCTTTCAGAGGGGAGCGGCTATCGGGGATG 489
QY      21 ProValAlaAsnGlySerProMetProLeuAlaProAlaAspAsnLeuArg---GlnAsp 39
        |||:::|||||
Db      490 CTTGTGGCTCTGGGGGCTATGCCCGCTCCCGCAGAGGAGAGAGAGAGAGAGAGAGAGAT 549
QY      40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTProArgThrLeuGlu 59
        |||:::|||||
Db      550 GCTCTCATTTGCTGGAATGTAGAGTGAGACCGGCTTCCAGACGTGGCAGACACCTGGAA 609
QY      60 ArgTyrProAspThrLeuLeuGlySerThrGluSerGluPhePheAsnGluAspThr 79
        |||:::|||||
Db      610 CGTACCCAGACACTTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669
QY      80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99
        |||:::|||||
Db      670 CAGCAGATATTTCTTGAACCGTGAACCAAGACATCTCCGCCACATCTCGAATTTCTACGC 729
QY      100 ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119
        |||:::|||||
Db      730 ACTGGGAAGCTCCACTATCTCTCGCAGAGAGGCACTCTCTTACGATGAAGAACTGGCC 789
QY      120 PheTyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGlyGlyTyrLysAspArg 139
        |||:::|||||
Db      790 TTTCTTGGCTCATCCCGGAATCATCGGCACACTGCTGTATAGGGAGTACAGAGATCGC 849
QY      140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnGlnGluSer 159
        |||:::|||||
Db      850 AGCGAGAGAACCGCGAGCGCTCGCAGAGACGACCGGATACCAACACCGCTGGGGAGACG 909
QY      160 --MetProSerLeuSerPheArgGlnThrMetTProAlaIlePheGluAsnProHisThr 178
        |||:::|||||
Db      910 GCCTTGCACCAACATGACGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 969
QY      179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
        |||:::|||||
Db      970 AGCAGATGCGCCGTGGTGTACTATGATCAAGGGAGTTTTCATGCGCTCGTGTATC 1029
QY      199 ThrAsnValIleGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
        |||:::|||||
Db      1030 GCGAATGTGTGGAACAGTGCCTGGGAGATCAAGCCAGGTCACTTAAAGAACTGCC 1089
QY      218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
        |||:::|||||
Db      1090 TGTGAGAGCGGTATGTGTGTGGCTTCTTGTGTGACACAGCGCTCGCATATATCTTC 1149
QY      238 ThrValGlyTyrLeuLeuArgLeuPheAlaIleProSerArgTyrArgPheIleArgSer 257
        |||:::|||||
Db      1150 ACAAGTGAATTTGCTTGGCTGCTGACGCGCTGAGCTTGTGCTTGTGCTGAGT 1209
QY      258 ValMetSerIleIleAspValAlaIleMetProTyrTyrIleGlyLeuValMetThr 277
        |||:::|||||
Db      1210 GTCTAGATATCATCGAGTGTGTGCTCTGCTTATTCATTTGGGCTGTGATGACA 1269
QY      278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
        |||:::|||||
Db      1270 GACATATGAGAGCGTCAAGGAGGAGCTTTGTGACATCCGAGCTTCCGGGCTTCAAGATC 1329
QY      298 PheLysPheSerArgHisSerGlnGlyLeuArgGlyLeuGlyTyrThrLeuLysSerCys 317
        |||:::|||||
Db      1330 TTTAAGTTTCCCGCACTTCAAGGCGCTGCAATCTCGGGGATACACATGAAAGATTGT 1389
QY      318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
        |||:::|||||
Db      1390 GCTTCAAAATTTGGGCTTCTTCTTCTGCTCAACATGGCTATCATCATCTTGGCTACA 1449

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Db      1146 CGTACCAGACACTTACTGGGACGTTGTGAGAGGAGACTTTTCTACCAACCAAGAACT 1205
Qy      80  LysGluTrPhePheAspArgPheProGluValPheArgCysValLeuAsnPheTrArg
      1206 CAGCAATATTTCTTTTACCGGTACCCAGACATCTTCGCGACATCTGTGAATTTCTACCGC 1265
Qy      100 ThrGlyLysLeuHisTrpProArgTrgGluCysIleSerAlaTrpAspArgGluLeuAla 119
      1266 ACTGGAGAGCTCCATCATCTCTCGCCACGAGTGATCTCTGCTTACATGAAAGCTGGGCG 1325
Qy      120 PheTrgGlyLLeuLeuProGluIleIleGlyAspCysCysTrgGluGluTrgIleAspArg 139
      1326 TTTTGGGCTCATCCCGGAAATCATCGGAGACTGCTGTTATGAGAGATCAAGATCGC 1385
Qy      140 LysArgGluAsnAlaGluArgLeuMetCysAspAspAspSerGluAsnAsnGlnIleSer 159
      1386 AGCGAGAGAGAACCCGACGCGCTCGACAGAGACGCGGATACCGACACCGCTGGGAGAGC 1445
Qy      160 --MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisTrh 178
      1446 GCCTTACCCACATGACTGCAGAGGAGAGGAGGCTTGAGAGGCGCTTCAGAAACCCCAAC 1505
Qy      179 SerThrLeuAlaLeuValPheTrgTrgValThrGlyPhePheIleAlaValSerValIle 198
      1506 AGCAGCATGGCCCTGGGTGTTCTACTAGTACGAGGATTTTTCATGCGCTCTGTGCATC 1565
Qy      199 ThrAsnValAlaGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
      1566 GCGAATGTGGTGAAGAACAGTGGCGGTGATCAAGGCCAGGATCACTTAAAGACTGCC 1625
Qy      218 CysGlyGluArgTrgSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
      1626 TGTGGAGAGGCTGATGTGGCTTCTTCTGCTTGAGACAGCGCTCGCTCATGATCTTC 1685
Qy      238 ThrValGluTrgLeuLeuArgLeuPheAlaAlaProSerArgTrgTrgPheIleArgSer 257
      1686 ACGGTGAGTATTTGCTTCCCTGGCTGCGACGCGCTAGTGTTACCGTTTGTGGCTAGT 1745
Qy      258 ValMetSerIleIleAspValAlaAlaIleMetProTrgTrgIleGlyLeuValMetThr 277
      1746 GTCATGATGATCATCAACGATGGTGGCCATCTGCTTATTACATTGGCGGTGGATGACA 1805
Qy      278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
      1806 GACAAATGAGGACGTCAGCGGAGCGCTTGTCACTCCGAGTCTTCGGGTCTTCAGAGATC 1865
Qy      298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTrpThrLeuLysSerCys 317
      1866 TTTTAAGTTTCCGCGCACTCTCAAGGCTGGCGATCTGGGTGACACACTGAAGATGTGT 1925
Qy      318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
      1926 GCGTCAGAAATTTGGGCTTCTGCTTCTCGCTCAACATGGCTATCATCTTCGCTTACA 1985
Qy      338 ValMetPheTrgAlaGluLysGlySerSerAlaSerIleAspPheThrSerIleProAlaSer 357
      1986 GTTATGTTCTACCGACAGAGAGGGGTCTTCGGCTAGAGATTCACGACATCCCTGCAGCC 2045
Qy      358 PheTrgTrgTrgTrgTrgIleValThrMetThrThrLeuGlyTrgGlyAspMetValProLysThr 377
      2046 TTTCTGATATCAATCGTCACATGACACACTGAGGTATGTATGATGATGGCCAAAACCC 2105
Qy      378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397
      2106 ATAGCAGAGAAATTTTGGTTCTATCTGTCCGTAGTGGGCTCTTGGCTATGCTCTTA 2165
Qy      398 ProValProValIleValSerAsnAspSerArgIleTrgHisGlnAsnGlnArgAlaAsp 417
      2166 CCGTGTCCGGTGAATGATCAACTTCAGTCGATCATCACACAGATCAACAGACAGAC 2225
Qy      418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437

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Db      2226 AAAGAAAGGCGACAAAGAAAGCTAGACTGGCCAGAGATCCGGGAGCCAAAGCGGAGC 2285
Qy      438 SerAsnAlaTrgLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457
      2286 GCAATGCTTATCATCGACAGCAAAAGGAAATGTTTACTGATATCAGTACGCTGCAG--TCC 2342
Qy      458 GlyThrProGluGluGluHisMetGlyLysMetGlyLysThrThrSerLeuIleGluSerGlnHis 477
      2343 TCAGAGATGAGCAGGCTTTTGTAGCAAAATCCGGCTCCAGCTTGTGAACCCAGCACAC 2402
Qy      478 HisLeuLeuHisCysLeuGluLysThrThrAsnHisGluPheIleAspGluIleMetPhe 497
      2403 CACCTGCTTCACTCCCTCGGAAAAACACGAAATCAGAGTTGTGGACGAGAAAGTCTT 2462
Qy      498 GlnGlnAsnCysMetGluSerSerMetGlnAsnTrpProSerThrArgSerProSerLeu 517
      2463 GAAGAAAGCTGATGAAAGTTGCAACTGTTAATGCTCTTCAAGTCAAGTCTTCACTG 2522
Qy      518 SerSerHisProGlyLeuThrThrThrCysCysSerTrgArgSerLysLysThrThrHis 537
      2523 TCTTCAACAAGAGATCACCAGACCTGCTGTTCAGACGACACAAAAAACCTTTTGGC 2582
Qy      538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnIleLeuSerThrIle 557
      2583 ATCCCAATGCCATGATATCAGAGAGCCATCAAGTATGATATACAGAACTCAAGACAT 2642
Qy      558 HisIleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLys 577
      2643 CAGATCAGATGTGTGGAGAGAACACTCTGTCTTAAACGCGGATCCAGTTTAAATGCCAA 2702
Qy      578 AlaAspAspGlyLeuAsnProAsnProAsnCysLysThrSerIleIleThrAlaIleIleSer 597
      2703 ATGAAAGTGTGTAAACTTAACTGTGAACAACCTTATGTGATGATACAGCAATATATAGC 2762
Qy      598 IleProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAla 615
      2763 ATCCCAACACTCCAGTACACACACAGAGAGAGATGAGCCAGAAATCCCGTGAATAC 2822
Qy      616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerVal 635
      2823 TCAGAGAGA-----AATATGTTCAGAGTTTCTGCT 2852
Qy      636 Leu 636
      2853 TTG 2855
Db
Qy
Db
RESULT 12
ADM10921
ID ADM10921 standard; cDNA: 5333 BP.
XX
XX ADM10921;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human O647SgenomicContig3 homologue cDNA #3.
DE
XX
XX ovastian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
KW cytosstatic; gene therapy; human; ss.
XX
XX Homo sapiens.
OS
XX
XX US2003206918-A1.
PN
XX
XX 06-NOV-2003.
PD
XX
XX 05-FEB-2003; 2003US-00361811.
PF
XX
XX 10-SEP-1999; 99US-00394374.
PR 01-MAY-2000; 2000US-00561778.
PR 15-AUG-2000; 2000US-00640173.
PR 07-SEP-2000; 2000US-00656668.
PR 14-NOV-2000; 2000US-00713550.
PR 03-APR-2001; 2001US-00825294.

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PR 02-OCT-2001; 2001US-00970966.  
 PR 02-AUG-2002; 2002US-00212677.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Fanger GR, Fling SP;  
 XX  
 DR WPI; 2003-901037/82.  
 DR P-PSDB; ADM10927.  
 XX  
 PT New polynucleotides encoding tumor proteins, treating or inhibiting the  
 PT development of cancer, particularly ovarian cancer, and for stimulating  
 PT and/or expanding T cells specific for a tumor protein.  
 XX  
 PS Example 12; SEQ ID NO 252; 221bp; English.

XX This invention describes a novel ovarian tumour protein which can be used  
 CC to detecting the presence of an ovarian cancer in a patient by  
 CC stimulating and/or expanding T cells specific for the tumour protein. The  
 CC products of the invention can also be used in a method to inhibit the  
 CC development of a cancer in a patient comprising (a) incubating CD4+  
 CC and/or CD8+ T cells isolated from a patient with at least one ovarian  
 CC tumour protein, such that T cell proliferate and (b) administering to the  
 CC patient the proliferated T cells. The cytostatic polynucleotides or  
 CC polypeptides described in the invention are useful for treating or  
 CC inhibiting the development of cancer, particularly ovarian cancer and for  
 CC stimulating and/or expanding T cells specific for a tumour protein or for  
 CC gene therapy.

XX Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4,16e-204 Length: 5333  
 Score: 2518.00 Matches: 486  
 Percent Similarity: 86.58% Conservative: 69  
 Best Local Similarity: 75.82% Mismatches: 70  
 Query Match: 75.84% Indels: 16  
 Gaps: 6

US-10-062-879-4 (1-636) x ADM10921 (1-5333)

QY 1 MetAlaIaGlyValAlaAlaATrPLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet 20  
 Db 966 ATGGCGGCGGGGGGCGGAGCGTGGCTTTTGCAGAGGCGAGCGGCTATGGGTGATG 1025  
 QY 21 ProValAlaAsnCySPrometProLeuAlaProAlaAspLyAsnLyAsp--GlnAsp 39  
 Db 1026 CCTGTGGCTTCGGGGGCTATGCGCGCTCCCGGAGGCGAGAGAGAAAGACCCAGAT 1085  
 QY 40 GlnLeuIleValLeuAsnValSerGlyArgArgPheGlnTrpArgThrThreuglu 59  
 Db 1086 GCTTCATGTGCTGGAATGTAGTGGACCGGCTTCCAGAGTGGACAGACCCCTGAA 1145  
 QY 60 ArgTyrProAspThrLeuLeuGlySerThrgluAspGluPhePheAsnGluAspThr 79  
 Db 1146 CGTTACCAACACACTCTACTGAGGAGTTCTTGAAGGAGACTTTTCTACACCCAGAAACT 1205  
 QY 80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99  
 Db 1206 CAGAGATATTTCTTTGACCGGACCCAGACATCTTCCGCACATCTCGAATTTCTACCGC 1265  
 QY 100 ThrGlyLysLeuHisTyrProArgTyrGluCysValLeuSerAlaTyrAspAspGluLeuAla 119  
 Db 1266 ACTGGAGAGCTCCATCTCCGCGACAGAGTCACTCTGCTTACGATGAAGAACTGGCC 1325  
 QY 120 PheTyrGlyLysLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArg 139  
 Db 1326 TTTCTTGGCCCTCATCCGGAAATCATCGGCGACTGCTTTATGAGAGTACAGAGATGCC 1385  
 QY 140 LysArgGluAsnAlaGluArgLeuMetCysAspAsnAspSerGluAsnAsnGlnGluSer 159  
 Db 1386 AGCGAGAGAAACCGCGCGCTCAGAGACGACCGCGATACCAACCGCTGGGAGAGGC 1445

QY 160 ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThr 178  
 Db 1446 GCTTGGCCACATGACATGACAGAGGGTCTGAGAGGCGCTTCGAGAAACCCACAGACC 1505  
 QY 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198  
 Db 1506 AGCAGATGGCGCTGGTGTCTACTATGTCAACGGGGTTTTTCATGTCCGTCTGTCTATC 1565  
 QY 199 ThrAsnValAlaGluThrValProCysGlyTyrValProGlySer---LysGluLeuPro 217  
 Db 1566 GCGAATGTGTGGAAACAGTCCCTGGGATCAAGCCAGTCACTTAAGAACTGGCC 1625  
 QY 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db 1626 TGTGAGAGCGGTATGTGTGTGCTTCTTCTGCTTGAACAGCGCTGGTATCATCTTC 1685  
 QY 238 ThrValGluTyrLeuLeuValGluPheAlaAlaProSerArgTyrArgPheIleArgSer 257  
 Db 1686 ACAGTTGAGATTTGTCTTGGCTTGGCTGCGACGCGCTTGTGCTTACCGTTTGTGCTGAT 1745  
 QY 258 ValMetSerIleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
 Db 1746 GTCAATGATATCATCGACGTGTGGCCATCTGCTTATTCATTTGAGGCTGTGTATGACA 1805  
 QY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297  
 Db 1806 GACATATGAGAGCGTCAACGGAGCCTTTGTCACTCCGAGCTTCGGGTCTTCAGGATC 1865  
 QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317  
 Db 1866 TTTAAGTTTTCCTCCCACTCCAGCGCTGGCATCTCTGGGTACACATGAAAGATTGT 1925  
 QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
 Db 1926 GCTTCAGAAATTTGGCTTCTTGTCTTCTTCTGTCACAAAGGTATCATCATCTTGTGATCA 1985  
 QY 338 ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357  
 Db 1986 GTTATGTCTTACGAGAGAAAGGGCTCTTCGGCTACGAAGTTACACACATCCCTGCAGGCC 2045  
 QY 358 PheTyrPyrThrIleValIleThrMetThrThreuglyTyrGlyAspMetValProLysThr 377  
 Db 2046 TTTCTGTATACATCGTCAACATGACAACTAGGGTATGTGTGATCATGTGCTCCAAAAC 2105  
 QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
 Db 2106 ATACAGAGGAGAAATTTTGTCTTATCTGTCTGTGAGTGGGCTTGTGATTTGCTCTTA 2165  
 QY 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417  
 Db 2166 CTTGTCCGATGTGTATTCACATTCAGTCGATCTACACCGAATCAACAGAGCAGAC 2225  
 QY 418 LysArgArgAlaGluLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437  
 Db 2226 AAACGAGGGGACAAAGAAAGTAACTGACGCGAGATCCGGGCGACCAAAAGCGAAGC 2285  
 QY 438 SerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
 Db 2286 GCAATCTTCAACAGAGACCAACGAAATGTATTACTAGTATCACTGACGTCGAC--TCC 2342  
 QY 458 GlyThrProGluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477  
 Db 2343 TCAGAGATAGACGCTTTTGTAGCAAAATCCGGCTCCAGCTTGTGAACCCAGACACAC 2402  
 QY 478 HisLeuLeuHisCysLeuGluLysThrThrAsnHisGluPheIleAspGluGlnMetPhe 497  
 Db 2403 CACCTGCTTCACTCCGTAAGAAACACAGATATCAAGATTGTGAGAGAAAGATCTTT 2462  
 QY 498 GlnGlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeu 517  
 Db 2463 GAAGAAAGCTGATGAGAAAGTTGCAACTGTTAATCTTCAATGATCAAGCTTCACTG 2522  
 QY 518 SerSerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysLysThrHis 537



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Db      2523 TCTTCACAGACGAGCAGCCACCTGCTGTTCACGACGACACAAAACCTTTGCC 2582
Qy      538 LeuProbsenSeranleuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle 557
Db      2583 ATCCCAATGCCAATGATATCATGAGACGACATCAAGATGATATACAAACCTCAGCAGAT 2642
Qy      558 HisIIGlnGlnSerGlnGlnProSerLeuThrThrSerArgSerSerLeuLeuLeu 577
Db      2643 CAGATCAGATGTGTGAGAGAACACCTCTGTCTTAACAGCCGATCCAGTTAAATGCCAAA 2702
Qy      578 AlaAspArgLeuArgProAsnCyblyThrSerGlnLeuThrThrAlaIleLeuSer 597
Db      2703 ATGAGAGAGTGTGTAACTAAACTGTGAACAACCTTATGTACTACAGCAATTAATAGC 2762
Qy      598 IleProThrProProAlaLeuThrProGlnGlnGluSerArgPro-----ProProAla 615
Db      2763 ATCCCAACACCTCCAGTAACCAACACGAGAGAGATGAGCCAGATCCCTGAGTAC 2822
Qy      616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValIysValSerVal 635
Db      2823 TCAGGAGGA-----AAATATGTCTAGAGATTCTGCT 2852
Qy      636 Leu 636
Db      2853 TTG 2855

RESULT 13
ADJ11253
ID      ADJ11253 standard; DNA; 5333 BP.
XX
AC      ADJ11253;
XX
DT      15-APR-2004 (first entry)
XX
DE      Human ovarian tumour antigen DNA Segid 254.
XX
KW      human; ds; ovarian cancer; immunogenic; antibody;
KM      antigen presenting cell; APC; immune system cell; T cell; tumorigenic;
XX      cytosolic; gene.
XX
OS      Homo sapiens.
XX
PN      US2003232056-A1.
XX
PD      18-DEC-2003.
XX
PF      14-FEB-2003; 2003US-00369186.
XX
PR      10-SEP-1999; 99US-00394374.
PR      01-MAY-2000; 2000US-00561778.
PR      15-AUG-2000; 2000US-00640173.
PR      07-SEP-2000; 2000US-00656668.
PR      14-NOV-2000; 2000US-00713550.
PR      03-APR-2001; 2001US-00825294.
PR      02-OCT-2001; 2001US-00970966.
PR      02-FEB-2002; 2002US-00212677.
PR      05-FEB-2003; 2003US-00361811.
XX
PA      (CORI-) CORIXA CORP.
XX
PI      Fanger GR, Fling SP;
XX
DR      WPI; 2004-178717/17.
XX      P-PSDB; ADJ11259.
XX
PT      Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
PT      polypeptide, useful as probes of primers for detecting presence of cancer
PT      in a patient.
XX
PS      Example 12; SEQ ID NO 254; 222pp; English.
XX
CC      This invention relates to novel isolated polynucleotides and methods for
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CC      the therapy and diagnosis of cancer, particularly ovarian cancer.
CC      Specifically, it refers to these polynucleotides and the encoded
CC      polypeptides thereof, as well as immunogenic peptides, antibodies,
CC      antigen presenting cells (APCs) and immune system cells (e.g. T cells)
CC      that are targeted to those cells expressing the proteins of interest. The
CC      present invention describes methods that are useful for stimulating and/
CC      or expanding T cells specific for a tumorigenic protein (i.e. T cell
CC      therapy). Furthermore, compositions can be used for the diagnosis,
CC      treatment and/or prevention of ovarian cancer by stimulating an immune
CC      response in a patient. Accordingly, these compositions exhibit cytotoxic
CC      activity. This polynucleotide is a human ovarian tumor antigen DNA
CC      sequence given in an exemplification of the invention.
```

SEQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	4,16e-204	Length:	5333
Score:	2518.00	Matches:	486
Percent Similarity:	86.58%	Conservative:	69
Best Local Similarity:	75.82%	Mismatches:	70
Query Match:	75.84%	Indels:	16
DB:	12	Gaps:	6

US-10-062-879-4 (1-636) x ADJ11253 (1-5333)

```
Qy      1 MetAlaAlaGlyValAlaAlaThrLeuProPheAlaArgAlaAlaIleGlyTrpMet 20
Db      966 ATGGCGGGGGGGGGGCGAGCGTGGCTGTTCAGAGAGGAGGCGCTATCGGGTGGATG 1025
Qy      21 ProValAlaAsnCybProMetProLeuAlaProAlaAspAsnIysArg---GlnAsp 39
Db      1026 CTTGGGCTCTGGGGGCGCTATCGGCTCCCGGAGGAGAGAGAGAGAGAGAGAGAGAGAT 1085
Qy      40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrLeuGlu 59
Db      1086 GCTCATTTGTTGTTGAATGATGATGAGGACCCGGCTTCAGACAGTGGACAGACCTCGAA 1145
Qy      60 ArgTyrProAspThrLeuLeuGlySerThrGluGlySerPhePheAsnGluAspThr 79
Db      1146 CGTTAACCCAGACACTCTAATCGGCGAGTTCGAGAGGAGACTTTTCTACACCCAGAAACT 1205
Qy      80 LysGluTyrPhePheAspArgAspProGluValPheArgCybValLeuAsnPheTyrArg 99
Db      1206 CAGCAGTATTTCTTTGACCGGACCGGACACATCTTCGCCACATCTGAAATTTCTACCGC 1265
Qy      100 ThrGlyLysLeuHisTyrProArgTyrGluCybIleSerAlaTyrAspAspGluLeuAla 119
Db      1266 ACTGGGAAGCTCCACTATCTCGCCACGAGGATCTCTGCTTACGATGAAGAACTGGCC 1325
Qy      120 PheTyrGlyIleLeuProGlnIleIleGlyAspCybCybTyrGluTyrLysAspArg 139
Db      1326 TTTCTTGGCTTCATCCCGGAATCATCGGCACTGCTTATGAGAGTACAAAGATCGC 1385
Qy      140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnIleSer 159
Db      1386 AGCGAGAGAAAGCGCGAGCGCTCGACAGACACCGGATACCAACACCGCTGGGGAGAGC 1445
Qy      160 ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThr 178
Db      1446 GCCTTGCCCAATGATGATCGAAGGAGGAGGCTCGAGAGGCGCTTCGAGAACCCCAACCC 1505
Qy      179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
Db      1506 AGCAGATGGCGCTGTGTCTTACTATGTCACGGGGTTCATTCATTCGCTGTGATC 1565
Qy      199 ThrAsnValIleGluThrValProCybGlyIleThrValProGlySer---LysGluLeuPro 217
Db      1566 GCGAATGTGTGAGAAACGTGCGGTGCGAGTCAAGCCAGGTCCATTAAGAACTGCGCC 1625
Qy      218 CysGlyGluArgTyrSerValAlaPhePheCybLeuAspThrAlaCysValMetIlePhe 237
Db      1626 TGTGAGAGCGGTATGCTGTGGCTTCTTCTGCTTGGACAGGCGCTCGTATATCTTTC 1685
```

QY 238 ThrValGlnTyrLeuLeuArgLeuPheAlaIleProSerArgTyrArgPheIleArgSer 257  
 Db 1686 ACAGTTAGATGTTGCTTCCCTGGCTGACGCTTACGCTTACCGTTTGGTGTGT 1745  
 QY 258 ValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
 Db 1746 GTCATGAGTATCATCGACGTGTGTGCTTCCTGCTTATCATGTTGGCTGTGTGCA 1805  
 QY 278 AsnAsnGluAspValSerGlyValAlaPheValThrLeuArgValPheArgIle 297  
 Db 1806 GACATATGAGACGTCAGCGAGGCTTGTCTACCTCCAGTCTTCCGGGCTTCCAGATC 1865  
 QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317  
 Db 1866 TTTTAAAGTTTCCGCCCATCTCCAGGCTGCGCATCTCGGGGTACACACTGAAGAGTTGT 1925  
 QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
 Db 1926 GCCCTCAGAAATGGGCTTCTTGTCTTCTCGCTCAACATGCTATCATCATCTCGCTACA 1985  
 QY 338 ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357  
 Db 1986 GTTATGTTCTACGAGAGAAAGGGCTTCCGCTAGCAAGTTCCACAGCATCTCCAGACC 2045  
 QY 358 PheTyrPyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377  
 Db 2046 TTCTGATATACCATCGTCACATGACAACTAAGGGATGTGTGACATGTGTCCAAAACC 2105  
 QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
 Db 2106 ATAGCAGGAGAAATTTTGGTTCTATCTGTTCCGCTGAGTGGGGCTTGGTCATGCTCTA 2165  
 QY 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417  
 Db 2166 CCGTTCCTCGGATGTATCCACTCATCTGATCTACCAACCAAGAACTCAAGCAGAC 2225  
 QY 418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437  
 Db 2226 AAGCGAAGGCGCAAAAGAAAGCTAGACTGCGCAGAGATCCGGGACCAAAAGCGGAAGC 2285  
 QY 438 SerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThr 457  
 Db 2286 GCAATATCTTACATGACAGCAAGAAAGGATGTTTACTCATGTAATCAGCTCAG---TCC 2342  
 QY 458 GlyThrProGluGluGluHisMetGlyLysThrThrSerLeuIleGlnSerGlnHis 477  
 Db 2343 TCAGAGAGTACGAGGCTTTTGTAGCAAAATCCGGCTCCAGCTTGAATCCACACACAC 2402  
 QY 478 HisLeuLeuHisCysLeuGluLysThrThrAsnHisGluPheIleAspGluGlnMetPhe 497  
 Db 2403 CACCTGCTTCACTCCCTGGAAAAAACACGAAATCAAGATTTGTGACGAAACAGTCTTT 2462  
 QY 498 GlnGlnAsnCysMetGlnSerSerMetGlnAsnTyrProSerThrArgSerProSerLeu 517  
 Db 2463 GAAGAAAGCTGACGAAAGTGTGCAACGTGTATATCGTCTTCAAGTACACAGCTTCACTG 2522  
 QY 518 SerSerHisProGlyLeuThrThrCysCysSerArgAspGlyLysThrThrHis 537  
 Db 2523 TCTTCAACAAAGAGATCACGACGCTGCTTCAAGACACCAAAAAAATCTTTCGC 2582  
 QY 538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle 557  
 Db 2583 ATCCCAATGCCAATGTATACGAAAGCATTAAGTATATACAAAGAACTACAGACGATTT 2642  
 QY 558 HisIleGlnGlySerGlnProSerLeuThrThrSerArgSerSerLeuAsnLys 577  
 Db 2643 CAGATCAGATGTGTGAGAGAAACACTCTGCTTAACAGCCATCAAGTTTAAATGCCAAA 2702  
 QY 578 AlaAspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrAlaIleIleSer 597  
 Db 2703 ATGGAAGAGTGTAAACTTAATGTAACCACTTATGACTTACAGCAATATATAGC 2762  
 QY 598 IleProThrProProAlaLeuThrProGluGlyLysSerArgPro-----ProProAla 615

Db 2763 ATCCCAACACCTCCAGTAAACCAACACAGAGAGACGATAGCCGATCCCTGAGTAC 2822  
 QY 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValLysValSerVal 635  
 Db 2823 TCAGAGAGA-----AAATATGTACAGATTTCTGCT 2852  
 QY 636 Leu 636  
 Db 2853 TTG 2855  
 RESULT 14  
 ADJ11251  
 ID ADJ11251 standard; DNA; 5333 BP.  
 XX  
 AC ADJ11251;  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Human ovarian tumour antigen DNA SegID 252.  
 XX  
 KW human; de; ovarian cancer; immunogenic; antibody;  
 KW antigen presenting cell; APC; immune system cell; T cell; tumourigenic;  
 KW cytostatic; gene.  
 XX  
 OS Homo sapiens.  
 EN US200322056-A1.  
 PD 18-DEC-2003.  
 XX  
 PE 14-FEB-2003; 2003US-00369186.  
 XX  
 PR 10-SEP-1999; 99US-00394374.  
 PR 01-MAY-2000; 2000US-00561778.  
 PR 15-AUG-2000; 2000US-00640173.  
 PR 07-SEP-2000; 2000US-00656668.  
 PR 14-NOV-2000; 2000US-00713550.  
 PR 03-APR-2001; 2001US-00825294.  
 PR 02-OCT-2001; 2001US-00870966.  
 PR 02-AUG-2002; 2002US-00212677.  
 PR 05-FEB-2003; 2003US-00361811.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Fanger GR, Fling SP;  
 XX  
 DR WPI; 2004-178717/17.  
 DR P-PSDB; ADJ11257.  
 XX  
 PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor  
 PT polypeptide, useful as probes of primers for detecting presence of cancer  
 PT in a patient.  
 XX  
 PS Example 12; SEQ ID NO 252; 222pp; English.  
 XX  
 CC This invention relates to novel isolated polynucleotides and methods for  
 CC the therapy and diagnosis of cancer, particularly ovarian cancer.  
 CC Specifically, it refers to these polynucleotides and the encoded  
 CC polypeptides thereof, as well as immunogenic peptides, antibodies,  
 CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)  
 CC that are targeted to those cells expressing the proteins of interest. The  
 CC present invention describes methods that are useful for stimulating and/  
 CC or expanding T cells specific for a tumourigenic protein (i.e. T cell  
 CC therapy). Furthermore, compositions can be used for the diagnosis,  
 CC treatment and/or prevention of ovarian cancer by stimulating an immune  
 CC response in a patient. Accordingly, these compositions exhibit cytostatic  
 CC activity. This polynucleotide is a human ovarian tumour antigen DNA  
 CC sequence given in an exemplification of the invention.  
 XX  
 SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;  
 Alignment Scores:

Pred. No.: 4,16e-204 Length: 5333  
 Score: 2518.00 Matches: 486  
 Percent Similarity: 86.58% Conservative: 69  
 Best Local Similarity: 75.82% Mismatches: 70  
 Query Match: 75.84% Indels: 16  
 DB: 12 Gaps: 6

US-10-062-879-4 (1-636) x ADU11251 (1-5333)

QY 1 MetAlaAlaGlyValAlaAlaTrpLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet 20  
 Db ATGGCGCGCGGGGTGGCAGCGTGGCTTTTGGCAAGGCGAGCGGCTATCGGGTGGATG 1025  
 QY 21 ProValAlaAsnCySPromecProLeuAlaProAlaAspLysAsnLysArg---GlnAsp 39  
 Db CCTGTGGCCCTCGGGGCGCTATGCGCGCTCCCGCCAGGCGAGAGGAAAAAGAACCCAAAGAT 1085  
 QY 40 GlnLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrLeuGlu 59  
 Db GCTCTCATTTGTCTGAATGATGATGGCACCCTTCACAGCTGGGAGACACCTCTGGAA 1145  
 QY 60 ArgTyProAspThrLeuLeuGlySerThrGlnLysGluPhePheAsnGlnAspThr 79  
 Db CGTACCCAGACACCTACTGGGCACTTCTGAGAGGAGACTTTTCTACCAACCAAGAAACT 1205  
 QY 80 LysGlnLysPhePheAspArgAspProGlnValPheArgCysValLeuAsnPheTyArg 99  
 Db CACAGATATTTCTTTGACCGTGACCCAGACATCTTCGCGCACATCTTGAATTTCTACCCG 1265  
 QY 100 ThrGlyLysLeuHisTyProArgTyArgLysCysIleSerAlaTyTrpAspGlnLeuAla 119  
 Db ACTGGGAAGCTCCACTATCTCGCCACAGATGATCTCTGCTTACATGAGAGAACTGGCC 1325  
 QY 120 PheTyGlyLysLeuProGlnIleIleGlyAspCysCysTyArgGlnLysArgLysAspArg 139  
 Db TTTCTTTGGCTTATCCCGGAATCATGCGGACTGCTGTTATGAGAGATCAAGATGCGC 1385  
 QY 140 LysArgGlnAsnAlaGlnLysLeuMetAspAspAsnAspSerGlnAsnAsnGlnLys 159  
 Db AGCGAGAGAAACCGCGCGCCCTGACGACGACGCGGATACCGACACCGCTGGGAGAGAC 1445  
 QY 160 ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGlnLysProHisThr 178  
 Db GCCTTGCCCAACATGATCGAACAGGAGGCTCTGAGGGCTTTCAGAAACCCCAACACC 1505  
 QY 179 SerThrLeuAlaLeuValPheTyTyTrpValThrGlyPhePheIleAlaValSerValIle 198  
 Db AGCAGCATGGCCCTGGTGTCTTACTATGTCACGGGGTTTTTTCATTCGCTCTGTCTATC 1565  
 QY 199 ThrAsnValValGlnThrValProCysGlyThrValProGlySer---LysGlnLeuPro 217  
 Db GCGAATGTGTGGAACACATGCGCGTGGGATCAAGCCCAAGGTCACTTAAAGAACTGCC 1625  
 QY 218 CysGlyGlnLysArgTySerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db TGTGGAAAGGAGTATGTGTGGCTTCTTGTCTTGACACGGCTGCGGTCAGATCTTC 1685  
 QY 238 ThrValGlnTyLeuLeuAspGlnPheAlaAlaProSerArgTyArgPheIleAspSer 257  
 Db ACAGTTGATTTTGTCTTCGCTGGCTGGCGACGGCTTATGTCGTTTGTGGCTAGT 1745  
 QY 258 ValMetSerIleIleAspValValAlaIleMetProTyTyTrpIleGlyLeuValMetThr 277  
 Db GTCATGTAGTATCATCGACGTGTGGCCATCTGCTTATTAACATTGGGCTGGATGACAC 1805  
 QY 278 AsnAsnGlnAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297  
 Db GACAAATAGAGACGTCAAGCGAGCGCTTTGTCAACTCGAATCTTCGGGGCTTCAGAGATC 1865  
 QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyTrpThrLeuLysSerCys 317  
 Db TTTAAGTTTTCGCCCACTCTCAAGGCTGCGCATCTGGGGTATCACACTGAAGAGTTGT 1925

QY 318 AlaSerGlnLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
 Db GCCTCGAATATTTGGCTTCTTGTCTTCTCTCAACATGGCATCATCATCTTCGCTACA 1985  
 QY 338 ValMetPheTyAlaGlnLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357  
 Db GTTATGTTTCAACGAGAGAGGGGTCTTCGGCTAGCAAGTTTCAACGATCCCTGGAGCC 2045  
 QY 358 PheTrpTyThrIleValThrMetThrThrLeuGlyTyTrpGlyAspMetValProLysThr 377  
 Db TTTGTGATATCCATCGTCAACATGACAACTAGGGATGTGTGACATGTGGCCAAAAACC 2105  
 QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
 Db ATACAGGAGAAATTTTGTCTTATCTGTTCGTGATGGGGCTTGTGTATTTGCTTA 2165  
 QY 398 ProValProValIleValSerAsnPheSerArgIleTyTrpIleGlnAsnGlnArgAlaAsp 417  
 Db CTTGTTCCGGTGAATTGTATTCAACTTCAGTCCGATCTACACAGATCAACAGAGCAGAC 2225  
 QY 418 LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437  
 Db AAACGAAGGCGCAAAAGAAAGCTAGACTGGCCAGATCCGGGCGACCAAAAGGGAAGC 2285  
 QY 438 SerAsnAlaTyTrpLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGlnLeuThr 457  
 Db GCAATGTCTTACAGCAGAGAAACGGAATGTTTACTCATGTAATCACTGCGAG---TCC 2342  
 QY 458 GlyThrProGlnGlnGlnHisMetGlyLysThrThrSerLeuIleGlnSerGlnHisHis 477  
 Db TCAGAGAGTAGAGCGCTTTTGTATGCAAAATCCGGCTCCAGCTTGAACCCAGACACAC 2402  
 QY 478 HisLeuLeuHisCysLeuGlnLysThrThrAsnHisGlnLysIleAspGlnLysMetPhe 497  
 Db CACCTGCTTCACTCCGCGGAAAAAACACGATACCAAGTTTGTGGACGAACAAGTCTT 2462  
 QY 498 GlnGlnAsnCysMetGlnLysSerMetGlnAsnTyProSerThrArgSerProSerLeu 517  
 Db GAAGAAAGCTCATGGAAGTTGCAACTGTTATATGCTCTTCAAGTCAAGTCTTCACTG 2522  
 QY 518 SerSerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysTyThrThrHis 537  
 Db TCTTCACAACAAGAGATCACAGACCTGCTTTCAGACGACACAAAAAATCTTTCGC 2582  
 QY 538 LeuProAsnSerAsnLeuProAlaIleThrArgLeuArgSerMetGlnLysLeuSerThrIle 557  
 Db ATCCCAATGCAATGATATCAGAAAGCCATCAAGGTAGTATACAAAGAACTCACACGATT 2642  
 QY 558 HisIleGlnGlySerGlnGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLys 577  
 Db CAGATCAATGTGTGGAGAGAACCTTGTCTTACAGCCGATCCAGTTTAAATGCCAAA 2702  
 QY 578 AlaAspAspGlyLeuArgProAsnCysLeuThrSerGlnIleThrThrAlaIleIleSer 597  
 Db ATGAAAGAGTGTAACTAACTGATGACAACTTATGATGATACGAAATATAAGC 2762  
 QY 598 IleProThrProProAlaLeuThrProGlnGlyGlnLysArgPro-----ProProAla 615  
 Db ATCCCAACACCTCCAGTAAACACACACAGAAAGAGACGATAGGCGCAATCCCTGAGTAC 2822  
 QY 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerVal 635  
 Db TCAAGAGGA-----AATATTTCAAGATTCTGCT 2852  
 QY 636 Leu 636  
 Db TTG 2855

RESULT 15

AD43512  
 AD43512 standard, DNA; 5333 BP.  
 AC AD43512;

XX 03-JUN-2004 (first entry)  
 XX Human ovarian cancer cDNA homologous DNA #6.  
 DE Human ovarian cancer; ovarian cancer; ovarian carcinoma; gene.  
 KW de; human; cancer; ovarian cancer; ovarian carcinoma; gene.  
 XX Homo sapiens.  
 XX US2003129192-A1.  
 PN 10-JUL-2003.  
 PD 02-AUG-2002; 2002US-00212677.  
 PF 10-SEP-1999; 99US-00394374.  
 PR 01-MAY-2000; 2000US-00561778.  
 PR 15-AUG-2000; 2000US-00640173.  
 PR 07-SEP-2000; 2000US-00656668.  
 PR 14-NOV-2000; 2000US-00713550.  
 PR 03-APR-2001; 2001US-00825294.  
 PR 02-OCT-2001; 2001US-00570366.  
 XX (CORI-) CORIXA CORP.  
 XX Chenault RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;  
 PI WPI; 2004-051070/05.  
 DR P-PSDB; ADM43518.  
 XX New isolated polynucleotide encoding an ovarian tumor protein for use in  
 PT diagnosing, preventing or treating cancer, particularly ovarian cancer.  
 PS Claim 1; SEQ ID NO 252; 220bp; English.  
 XX The invention relates to an isolated polynucleotide. The invention is  
 CC used to diagnose, prevent or treat cancer, particularly ovarian cancer.  
 CC The present sequence represents a human ovarian carcinoma cDNA homologous  
 CC DNA.  
 SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 4,16e-204 Length: 5333  
 Score: 2518.00 Matches: 486  
 Percent Similarity: 86.58% Conservative: 69  
 Best Local Similarity: 75.82% Mismatches: 70  
 Query Match: 75.84% Indels: 16  
 Gaps: 6  
 DB: 12  
 US-10-062-879-4 (1-636) x ADM43512 (1-5333)  
 QY 1 MetAlaAlaGlyValAlaAlaATPLeuProPheAlaArgAlaAlaAlaGlyTyrMet 20  
 Db ATGGCGGGGGCGTGGCGGCTGCTTTTCAAGGCGGCGGCTATGGGTGATG 1025  
 QY 21 ProValAlaAsnCySPrometProLeuAlaProAlaAspIysAsnIyAsp---GlnAsp 39  
 Db CCTGTGCTCTGGGGCTATGCTCCCGCTCCCGGAGGCGAGAGAAAGAACCAAGAT 1085  
 QY 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTyrPargThrThreGlu 59  
 Db GCTCTATTGTGCTGAATGTGATGGCACCGCTTCCAGACGTGGCAGAACCTTGGA 1145  
 QY 60 ArgTyrProAspThrIleuLeuGlySerThrGluIlysgIuPhePheAsnGluAspThr 79  
 Db 1146 CGTAAACCAAGACACTACTGCGAGTTCGAGAGGAGCTTTTCTACACCAAGAACT 1205  
 QY 80 LysGluIlyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99  
 Db 1206 CAGAGATATTTCTTTGACCGGACCCAGACATCTTCCGCCACATCTGAAATTTCTACGC 1265  
 QY 100 ThrGlyLysLeuHistyTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119

Db 1266 ACTGGAAAGCTCCACTATCCCTGCGACAGAGGCATCTCTGCTTGCATGAGAACTGGCC 1325  
 QY 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArg 139  
 Db 1326 TTTCTTGCTCTATCCCGAAATCATCGGACCATGCTGTATATGAGAGTACAAAGATCGC 1385  
 QY 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnGluIlyser 159  
 Db 1386 AGCGAGAGAAACCGCGAGCGCTTCAGAGACGACCGGATACCAACCCGCTGGGAGAGC 1445  
 QY 160 ---MetProSerLeuSerPheArgGlnThrMetTyrAlaPheGluAsnProHisThr 178  
 Db 1446 GCTTGCCCAACCATGACTGACAGGAGGAGGCTGTGAGAGGCGCTTCGAGAACCCACACCC 1505  
 QY 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198  
 Db 1506 AGCAGATGGCGCTGGGTCTTACTATGTCAACGGGATTTTTCATGTGCGTCTGTATC 1565  
 QY 199 ThrAsnValAlaGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217  
 Db 1566 GCGAATGTGTGAGAAACAGTCCCTGCGGATCAAGCCAGGTCACTTAAGAACTGCGCC 1625  
 QY 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
 Db 1626 TGTGAGAGCGGTATGTGTGTGCTTCTGCTTGTGACACAGCGCTCGTATGATCTTC 1685  
 QY 238 ThrValGluTyrIleLeuAlaArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257  
 Db 1686 ACAGTTAGATATTTGCTTCCCTGCGTGGCAGCGCTGATGCTTATCCGTTTGTGCTGAT 1745  
 QY 258 ValMetSerIleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
 Db 1746 GTCAATGATATCATCGACGTGTGGCCATCTGCTTATTCATTTGGGCTGTATGACA 1805  
 QY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297  
 Db 1806 GACAAATGAGGACGTCACAGGAGCTTTGTCACTCCAGATCTCCGGCTTCAAGATC 1865  
 QY 298 PheIysPheSerArgIleSerGlnGlyLeuArgIleLeuGlyTyrThrLeuIlySerCys 317  
 Db 1866 TTTAAGTTTTCCTCCCTCACTCAAGGCTCGCTGAGCTGAGTCAACATCGAAGAGTGT 1925  
 QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr 337  
 Db 1926 GCTTCAAAATTTGGCTTCTTGTCTTCTCGTCAACATGGCTATCATCATCTTGGCTACA 1985  
 QY 338 ValMetPheTyrAlaGluIlysgIySerSerAlaSerIlyspPheThrSerIleProAlaSer 357  
 Db 1986 GTTATGTCTTACGAGAGAGGGGTCTTGGCTAGCAAGTTCAACACATCCCTCGAGCC 2045  
 QY 358 PheTyrTyrThrIleValThrMetThrThreGluIlyrGlyAspMetValProIyThr 377  
 Db 2046 TTTCTGTATACATCTGTCACATGACAACTAGGGTATGTGACATGAGTCCAAAAACC 2105  
 QY 378 IleAlaGlyIlyIlePheGlySerIleCysSerIleuSerGlyValLeuValIleAlaLeu 397  
 Db 2106 ATAGCAAGAGAAATTTGTGTTCTATCTGTTCGTGAGTGGGCTTGTGATCTTCTTA 2165  
 QY 398 ProValProValIleValSerAsnPheSerArgIleTyrIleGlnAsnGluArgAlaAsp 417  
 Db 2166 CTTGTCGGGAGTATGATCACTTCACTTCAGTCGATCAACCAAGATCAACGAGCAAGC 2225  
 QY 418 LysArgArgAlaGluIlyIlyValAlaArgLeuAlaArgIleArgValAlaIlyThrGlySer 437  
 Db 2226 AAACGAAAGGACACAAAAGAAAGCTAGACTGCGCAGATCCGGCGAGCAAAAGGGAAGC 2285  
 QY 438 SerAsnAlaTyrIleuHisSerIlyArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
 Db 2286 GCATATCTTACATGACAGAGCAAGAGATGGTTTATCTCACTGATATCAGCTGCAAG---TCC 2342  
 QY 458 GlyThrProGluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477

Db 2343 TCAGAGATAGACAGGCTTTTGTAGCAATCCGGCTCCAGCTTTGAAACCCAGACAC 2402  
Qy 478 HisleuLeuHisCysLeuGluLeuGluLeuThrThrAsnHisGluPheLeuLeuGluMetPhe 497  
Db 2403 CACCTGCTTCACTGCTCGGAAAAAACCAAGATCAAGATTTGTGACGACCAAGCTTT 2462  
Qy 498 GluGlnAsnGlyMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeu 517  
Db 2463 GAGGAAAGCTGACATGAGGATTCGACCTGTTAATGCTTCAAGTCAAGTCTCTTACG 2522  
Qy 518 SerSerHisProGluLeuThrThrThrThrCysCysSerArgArgSerHisLeuThrHis 537  
Db 2523 TCTTCAACAAGAGAGTACACAGACCTGCTGTTTCAAGACAGACAAAACCTTTTCC 2582  
Qy 538 LeuProAsnSerArgLeuLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle 557  
Db 2583 ATCCCAATGCTCAATGATATGACAGAGCCATCAAGTATGATTAACAAGACTCAGACGATT 2642  
Qy 558 HisLeuGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLeu 577  
Db 2643 CAGATCAGATGTGTGAGAGAAACCTCTGTCTTAACGCGATCCAGTTTAAATGCCAA 2702  
Qy 578 AlaAspArgLeuArgProAsnCysLeuThrSerGlnLeuThrThrAlaIleIleSer 597  
Db 2703 ATGGAAGAGTGTATAACTTAACCTGGAACAACCTTATGCTACAGCAATATATAC 2762  
Qy 598 IleProThrProProAlaLeuThrProGluGluGluSerArgPro-----ProProAla 615  
Db 2763 ATCCCAACACCTCAGATACCAACCAAGAGACATGAGCCAGAAATCCCTGAGTAC 2822  
Qy 616 SerProGluProAsnThrAsnIleProSerIleThrSerAsnValIleValSerVal 635  
Db 2823 TCAGAGAGA-----AAATATGTCAAGATTTCTGCT 2852  
Qy 636 Leu 636  
Db 2853 TTG 2855

RESULT 16  
ADM43514  
ID ADM43514 standard; DNA; 5333 BP.  
XX  
AC ADM43514;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human ovarian cancer cDNA homologous DNA #8.  
XX  
KW de; human; cancer; ovarian cancer; ovarian carcinoma; gene.  
XX  
OS Homo sapiens.  
XX  
PN US2003129192-A1.  
XX  
PD 10-JUL-2003.  
XX  
PF 02-AUG-2002; 2002US-00212677.  
XX  
PR 10-SEP-1999; 99US-00394374.  
PR 01-MAY-2000; 2000US-00561778.  
PR 15-AUG-2000; 2000US-00640173.  
PR 07-SEP-2000; 2000US-00656668.  
PR 14-NOV-2000; 2000US-00713550.  
PR 03-APR-2001; 2001US-00825294.  
PR 02-OCT-2001; 2001US-00970966.  
XX  
PA (COR-) CORIXA CORP.  
XX  
PI Chenaule RA, Xu J, Fanger GR, Harlocker SL, McNeill PD;  
XX  
DR WPI: 2004-051070/05.  
XX  
DR P-PSDB; ADM43520.  
XX

PT New isolated polynucleotide encoding an ovarian tumor protein for use in  
diagnosing, preventing or treating cancer, particularly ovarian cancer.  
XX  
PS Claim 1; SEQ ID NO 254; 220pp; English.  
XX  
XX  
CC The invention relates to an isolated polynucleotide. The invention is  
used to diagnose, prevent or treat cancer, particularly ovarian cancer.  
CC The present sequence represents a human ovarian carcinoma cDNA homologous  
DNA.  
XX  
SQ Sequence 5333 BP; 1510 A; 1136 C; 1167 G; 1520 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 4.16e-204 Length: 5333  
Score: 2518.00 Matches: 486  
Percent Similarity: 86.58% Conservative: 60  
Best Local Similarity: 75.82% Mismatches: 79  
Query Match: 75.84% Indels: 16  
DB: 12 Gaps: 6  
US-10-062-879-4 (1-636) x ADM43514 (1-5333)  
Qy 1 MetAlaAlaGlyValAlaAlaTrpLeuProPheAlaArgAlaAlaAlaIleGlyTyrMet 20  
Db 966 ATGGCGGGGGGGGTGGAGCGCTGCTGCTTTTCAAGGCGAGCGCTATCGGGTGGATG 1025  
Qy 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspIleValArg--GlnAsp 39  
Db 1026 CCTGTGGCTCGGGGGCTTATCCGGCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1085  
Qy 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrLeuGlu 59  
Db 1086 GCTTCATTTGCTGAATGATGAGTGCAACCGCTTCCAGACGAGGAGGAGGAGGAGGAGGAGG 1145  
Qy 60 ArgTyrProAspThrLeuLeuGlySerThrGluLeuGluPhePheAsnGluAspThr 79  
Db 1146 CGTTACCCAGACACTCTACCTGCGAGTCTGAGAGGACTTTTCTACACCCAGAAACT 1205  
Qy 80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99  
Db 1206 CAGCAGTATTTCTTGTGACCGTGACCCAGACATCTTCCGCCACCTGAAATTTCTACCGC 1265  
Qy 100 ThrGlyLeuLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119  
Db 1266 ACTGGGAAGCTCCACTATCTCTGCGACGAGGACATCTCTGTTCAGATGAGAACTGACC 1325  
Qy 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLeuAspArg 139  
Db 1326 TTCTTTGGCTCTATCCCGGAATCATCGGCCACTGCTTATGAGAGTACAGAGATCGC 1385  
Qy 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnIleSer 159  
Db 1386 AGCGAGAGAGAACGCGGAGCGCTCAGAGGACGACCGGATACCGACCGCTGGGAGAGGC 1445  
Qy 160 ---MetProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThr 178  
Db 1446 GCCTTGGCCACATGACATGCAAGGACAGAGGTCTGAGAGGCTTCGAGAACCCCAACACC 1505  
Qy 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198  
Db 1506 AGCAGAGATGCGCTGCTGTCTTACTATGTCACGGGGTTTTCATTCGCTCTGTATC 1565  
Qy 199 ThrAsnValAlaGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217  
Db 1566 GCGAATGTGTGAGAAAGTGCCTGCGGATCAAGCCAGGTCACATTAAGAAGCTGCC 1625  
Qy 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237  
Db 1626 TGTGAGAGCGGTATGCTGTGCTTCTTCTGCTTGAACAGGCGCTCGCATATCTTC 1685  
Qy 238 ThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257  
Db 1686 ACAGTTGAGTATTTGCTTGGCTGCTGCGCTGACGCGCTTACCGTTTGTGCGGATG 1745

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Qy 258 ValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThr
Db 1746 GTCAATGATATCATCGAGTGGTGGCATCTCGCTTATTCATTGGGCTGGTATGACA 1805
Qy 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgIle 297
Db 1806 GACAAATGAGGAGCTGAGGAGGCTTGTCACTCCAGACTTCCGGGCTTCAGAGATC 1865
Qy 298 PheArgPheSerArgHisSerGlnGlyLeuArgIleLeuArgIleTyrThrLeuLeuSerCys 317
Db 1866 TTTAAGTTTCCCGCACTCCAGGCTCGGAGCTCGGAGTACACCTGAAGGTGT 1925
Qy 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr 337
Db 1926 GCCCAGAAATGGGCTTCTGCTTTCGCTCACCAATGCTATCATATCTCGCTACA 1985
Qy 338 ValMetPheTyrAlaGluLeuGlySerSerAlaSerIlePheThrSerIleProAlaSer 357
Db 1986 GTTATGTTCTACGAGAGAAAGGCTTCGGCTAGCAAGTTTACACAGCATCCCTGACACC 2045
Qy 358 PheTyrPyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIleThr 377
Db 2046 TTCTGATATACATCGTCACCATGACAACTAGGATATGGTACATGGTCCAAAACC 2105
Qy 378 IleAlaGlyLeuIlePheGlySerIleCysSerLeuSerGlyValIleValIleAlaLeu 397
Db 2106 ATAGCAGGAGAAATTTTGGTTCATCTGTTCCGTCAGTGGGCTTGGTATGCTCTTA 2165
Qy 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417
Db 2166 CTTGTCGGGTGATGTATCACTTCACTGATCTTACCAACCAAGATCAACGAGCAGAC 2225
Qy 418 LysArgArgAlaGlnIleLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437
Db 2226 AAACGAAAGGACAAAGAAAGCTAGACTGCGCAGAGATCCGGGACGCCAAAAGCGAAGC 2285
Qy 438 SerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457
Db 2286 GCAAATCTTATCATCGAGCAGCAACGAAATGGTTTACTCATGATACAGCTCAG--TCC 2342
Qy 458 GlyThrProGluGluGlnHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHis 477
Db 2343 TCAGAGATGAGCAGGGCTTTTGTAGCAAAATCCGGCTCAGCTTGAACCAACAGACAC 2402
Qy 478 HisLeuLeuHisCysLeuGluLysThrThrAsnHisGluPheIleAspGluGlnMetPhe 497
Db 2403 CACCTGCTTCACTGCTCGAAGAAAACCAAGATCAGAGTTGTGAGCAAGATGCTTT 2462
Qy 498 GlnGlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeu 517
Db 2463 GAAGAAAGCTGCAGAGAGTTGCAACTGTTATGTCCTTCAACTCAAGCTCTTCACTG 2522
Qy 518 SerSerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysLysThrHis 537
Db 2523 TCTTCAACAAGAGATGACACAGACCTGCTTACAGACACACAAAACCTTTCCG 2582
Qy 538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnLeuLeuSerThrIle 557
Db 2583 ATCCCAATGCCAATGATATCAGAAAGCATCAAGTGTATTAACAAGAACTCAGACAGATT 2642
Qy 558 HisIleGlnGlySerGlnGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLys 577
Db 2643 CAGTTCGATGTGTGAGAGAACCTCTGTCTACAGCCATCCAGTTTAAATGCCAAA 2702
Qy 578 AlaAspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleIleSer 597
Db 2703 ATGGAAGAGTGTATAAAGTAACTGAACGTGAACAACCTTATGATACAGCAATATAAGC 2762
Qy 598 IleProThrProProAlaLeuThrProGluGlyLysSerArgPro-----ProProAla 615
Db 2763 ATCCCAACACCTCCAGTAAACACACAGAAAGAGACGATGAGCCAGAAATCCCTGAGTAC 2822

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Qy 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerVal 635
Db 2823 TCAGAGAGCA-----AAATATGTCAGAGTTTCTGCT 2852
Qy 636 Leu 636
Db 2853 TTG 2855

RESULT 17
ADP21361
ID ADP21361 standard; DNA; 5333 BP.
XX
AC ADP21361;
XX
DT 09-SEP-2004 (first entry)
XX
DE Gene KCND2 for screening for cardiac therapeutic preparation.
XX
KW ds; cardiant; gene therapy; cardiac therapeutic preparation;
KW beta-adrenergic receptor antagonist; endothelial receptor antagonist;
KW calcium channel antagonist; phosphodiesterase inhibitor;
KW angiotensin converting enzyme inhibitor; heart failure.
XX
OS Homo sapiens.
XX
PM W02004050894-A2.
XX
PD 17-JUN-2004.
XX
PE 26-NOV-2003; 2003WO-US037927.
XX
PR 27-NOV-2002; 2002US-0429379P.
PR 31-DEC-2002; 2002US-0437051P.
PR 31-DEC-2002; 2002US-0437102P.
XX
PA (ARTE-) ARTESIAN THERAPEUTICS INC.
XX
PI Bednarik DP;
XX
DR WPI; 2004-450738/42.
XX
PT Screening potential therapeutic compounds for cardiac therapeutic
PT preparations, useful for treating heart failure in a subject, comprises
PT contacting a sample of cell or tissue with a compound and detecting gene
PT expression level.
XX
PS Claim 10; SEQ ID NO 35; 152bp; English.
XX
CC The invention relates to a method of screening potential therapeutic
CC compounds for cardiac therapeutic preparations by contacting a sample
CC comprising a cell or tissue with a potential therapeutic compound and
CC detecting a level of expression of a gene that codes for a product
CC encoded by a nucleic acid selected from 98 sequences given in the
CC specification and its conservative variants, comparing the level of the
CC expression of the gene to the level of expression of the gene in the
CC absence of the compound, and identifying a potential therapeutic compound
CC for use as a cardiac therapeutic preparation if the potential therapeutic
CC compound affects the level of expression of the gene. The pharmaceutical
CC composition or active agents (i.e., beta-adrenergic receptor antagonist,
CC endothelial receptor antagonist, calcium channel antagonist,
CC phosphodiesterase inhibitor, or angiotensin converting enzyme inhibitor)
CC is useful for treating heart failure in a subject. This sequence
CC represents one of the genes whose expression may be altered by the
CC compounds detected by the screen of the invention.
XX
SQ Sequence 5333 BP; 1509 A; 1136 C; 1167 G; 1521 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.: 4,16e-204 Length: 5333
Score: 2518.00 Matches: 486
Percent Similarity: 86.58% Conservative: 69
Best Local Similarity: 75.82% Mismatches: 70
Query Match: 75.84% Indels: 16

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KM Human; Kv4.1, potassium channel protein; Kv4.2, autism; epilepsy;  
 KM neurodegenerative disease; ischemia; stroke; Alzheimer's disease;  
 KM Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;  
 KM learning capacity; protein kinase activator; anti-arrhythmic; ss.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH CDS 84..2024  
 FT /\*tag= a  
 FT /product= "Kv4.1 alpha subunit"  
 XX DE19963612-A1.  
 XX 12-JUL-2001.  
 XX 29-DEC-1999; 99DE-01063612.  
 XX 29-DEC-1999; 99DE-01063612.  
 XX (GENT-) FORSCHUNGSGESELLSCHAFT GENION MBH.  
 XX WPI; 2001-426637/46.  
 XX P-PSDB; AAB86318.  
 PT New potassium channel subunit proteins, useful for identifying and  
 PT testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological  
 PT agents.  
 XX Claim 11; Page 13-16; 50bp; German.  
 CC This invention describes a novel potassium channel protein (I) that is  
 CC either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium for  
 CC channels containing (I) are used to identify and test: (i) compounds for  
 CC treatment of neurodegenerative diseases (autism, epilepsy, ischemia,  
 CC stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac  
 CC arrhythmia, or those that improve learning capacity and memory; and (ii)  
 CC activators of protein kinases. Host cells that express (I) can identify  
 CC agents that do not interact significantly with channels and control I\_c\_o  
 CC (a quickly activated transient current), so lack the side effects of  
 CC known anti-arrhythmic agents. They also eliminate, or reduce, the need  
 CC for testing on organ cultures  
 XX SO Sequence 2711 BP; 528 A; 867 C; 737 G; 579 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.28e-171 Length: 2711  
 Score: 2132.50 Matches: 430  
 Percent Similarity: 77.24% Conservative: 79  
 Best Local Similarity: 65.25% Mismatches: 115  
 Query Match: 64.23% Indels: 35  
 DB: 4 Gaps: 13  
 US-10-062-879-4 (1-636) x AAH21246 (1-2711)  
 QY 1 MetAlaAlaGlyValAlaAlaTPrLeuProPheAlaArgAlaAlaAlaIleGlyTTPMet 20  
 DB 81 ATGGCGGACAGCGCTGCGCAGTGGCTCTTTTCTCGGCGAGACAGAGTGGCTGCTG 140  
 QY 21 ProValAlaAspCysProMetProLeuAlaProAlaAspLysAsnLysArgGluAspGlu 40  
 DB 141 CCCTTGGCCCGACCAACCCCTGCCCGCGGACCGGGGTGAAGGATCTCCAGAGATGAG 200  
 QY 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrThrPargThrThrLeuGluArg 60  
 DB 201 GTTCTGTGTGTGAACGTGAGCGAGCGGCTTTAGACTTGAAGAAATACCGTGAACGCG 260  
 QY 61 TyrProAspThrLeuLeuGlySerThrGluArgGluPhePhePheAsnGluAspThrLys 80  
 DB 261 TACCAAGACACCTTCTGGGCGAGCTCGAGAGAGAAATTTCTTTCAGATGCTGACCTGAGC 320  
 QY 81 GluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100

Db 321 GAGTACTTCTTCATCGCAGCCCTGACATGTTCCGCCATGCTGAACTTCTACCGAAG 380  
 QY 101 GlyValLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
 Db 381 GGGCGGCTGATGCCAGCGAGAGTGAATCCAGGCTTTCGACGAGAGAGCTGGCTTTC 440  
 QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArgLys 140  
 Db 441 TACGGCTGTGTTCCCGAGTACTAGTGGTGAAGTGGCTTGAAGAGTATCGGAGCGAAG 500  
 QY 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGluSerMet 160  
 Db 501 AAGGAGATGCGCAGCGCTGCGCAGAGATGAGGACAGAGCGCGCGGAGCGGC--- 557  
 QY 161 ProSerLeu-----SerPheArgGlnThrMetTPrPargAlaPheGluAsnPro 176  
 Db 558 CCAGCCCTGCGCAGCAGCAGCTCCCTGCGGAGCGGCTGCGGCGGCTTGAAGATCCA 617  
 QY 177 HisThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSer 196  
 Db 618 CACACGAGCACCCGAGCGCTGTTTCTACTATGTGACCGGCTTCTCATGCGCGTGG 677  
 QY 197 ValIleThrAsnValValGluThrValProCys-----GlyThrValProGlySerLys 214  
 Db 678 GTCATGCCCAATGTGTGAGAGACCATCCATGCCGCGCTCTGACGACGAGTCTCTCAAG 737  
 QY 215 GluLeuProCysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysVal 234  
 Db 738 GAGAGCGCTGTGCGAAGCCTTCCACAGGCTTTTGTGATGACAGACAGCTGTGTA 797  
 QY 235 MetIlePheThrValGluTyrLeuLeuArgLeuPheAlaIleProSerArgTyrArgPhe 254  
 Db 798 CTCATATTCACAGGTGAATATCTCTGCGCTGTTCCGCCGCCACCGCTGGCGCTTC 857  
 QY 255 IleArgSerValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeu 274  
 Db 858 CTGGGAGGTGTCATGAGCTCATGAGCTGTGGCCATCTGCCCTACTCATATGGGCTT 917  
 QY 275 ValMetThrAsnAsnGluAspValSerGlyValaPheValThrLeuAlaValPheArgVal 294  
 Db 918 TTGTGTGCCAAGACAGACATGCTCTGCGGCTTTGTGATCAACCTGCTGTGTCCGGGTG 977  
 QY 295 PheArgIlePheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeu 314  
 Db 978 TTTCGATCTTCAAGTCTCTCAGGACTCACAGGCTTGAAGATTCGGGCTACACATC 1037  
 QY 315 LysSerCysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIle 334  
 Db 1038 AAGAGCTGTGCTGTGAGTGGGCTTCTCTCTTTCCCTAACCATGCGCATCATCATC 1097  
 QY 335 PheAlaThrValMetPheTyrAlaGluGlySerSerAlaSerLysPheThrSerIle 354  
 Db 1098 TTGTGCCACTGTCAATGTTTATGCTGAGAGAGGACAAACAAACCACTTACAGATC 1157  
 QY 355 ProAlaSerPheThrTyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetVal 374  
 Db 1158 CTGGGCGCTTCTGGATATACATTTGTCACATGACACAGCTTGGCTACGAGACATG 1217  
 QY 375 ProLysThrIleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuVal 394  
 Db 1218 CCAGACACCATTTGTGTGCAAGATTTTGGGTTCATGCTCATGATGGCGTCTTGTC 1277  
 QY 395 IleAlaLeuProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGln 414  
 Db 1278 ATTGCCCTGCTGTGCCAGTCAATGTGTCCAACTTTAGCCGCACTTACACACAGAAC 1337  
 QY 415 ArgAlaAspLysArgArgAlaGlnLysLysValArgLeuAlaArgIleArgValAlaLys 434  
 Db 1338 CGGGCTACAGCGCCGAGACAGACAGAGAGTGGCTTGGCAGAGATCCGGTTGGCAAG 1397  
 QY 435 ThrGlySerSerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeu 454  
 Db 1398 AGTGTATCACCAATGCTTCTGCGAGTACAAAGCAGATATGG-----GGCCTT 1445



Oy	455	Glut1erThrglyThrProGluGluIuhismet---GlyLythrThrSerLeuileGlu	473
Db	1446	GAGACACGGCAGAGTGGGAGGACAGAGCTCTTGTGTACAGAACCGTTTCCTGTTGAA	1500
Oy	474	SerGlnIshIshIshLeuLeuIshCysLeuGulLythrThrAsnIshGluIhe1LeaP	493
Db	1506	CAGCAACATCAACCACTTGCTGTGACTGTCTAGAGAGAACACGTCCATGATTCACAGAT	1565
Oy	494	GluGlnMetPheGluGlnAsnCysMetGluSerSerMetGlnAsnTyPProserThrxg	513
Db	1566	GAGCTCACCTTCAGTGAA--GCCCTGGAGCGGCTGTGCGCGGGTGGCCGACACAGCGT	1622
Oy	514	SerProSerLeuSerSerIshPro-----GlyLeuThrThrCysCysSer	529
Db	1623	AGCAACCTGTGTGTCTTCCACAGCAATGGGAGACCCGGAGCGTGTGTCTTGTGTCGCCCT	1682
Oy	530	ArgArgSerLyS--LyserThrThrIshLeuProAsnSerAsnLeuProAlaThrArgLeu	548
Db	1683	CGCAGGGCGCAAGCGCGCGCCATCCGCTTGCCCACTCCACATGCTCAGTCAAGCCGT---	1733
Oy	549	ArgserMetGlnGluLeuSerThrIleIshIleGlnGlyserGluGlnProserLeuThr	568
Db	1740	GGCAGCAATGACAGAGACTGTGACATG-----CTGGAGGGGCTGGCAGAGACCATGCCCCCT	1792
Oy	569	ThrSerArgSerSerLeuAsnLeuIshAlaAspArgGlyLeuArgProAsnCysLyserThr	588
Db	1794	CAGACGGCTCCAGCTCATATGCCAAGGCCCATGACAGCTTGACCTGAATCGCAGCAGC	1852
Oy	589	SerGlnIleThrAlaIleIshSerIleProThrProProAlaLeuThrProGluGly	608
Db	1854	CGGACCTTCGTGGCTGCATTTATGACATCCCTACCCCTCTGCGCAACACCCACAGAT---	1910
Oy	609	GluSerArgProProProAlaSerProGly-----	618
Db	1911	GAGAGCCGAA-----CCTTCCTCCCTGCGCGCGGTGGCAGGCGCGCAGCACCCCTCAGG	1962
Oy	619	---ProAsnThrAsnIshProSerIleThrSerAsnValIshValSerValIsh	636
Db	1965	AACCTCAGCGCTGGGACCCCTTGCTGCTTCCCGCAGACGTGTCAGATCTCATCCCTGG	2021
RESULT 19			
AAZ11901	ID	AAZ11901 standard; cDNA; 3424 BP.	
XX	AC	AAZ11901;	
XX	DT	30-NOV-1999 (first entry)	
DE		Human potassium channel K+Hnov12 cDNA.	
XX	KW	Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;	
KW	KW	cardiovascular disorder; CNS disorder; renal disorder; ds.	
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
FT	FT	CDS 257..2195	
FT	FT	/tag= a	
FT	FT	/product= "Human K+Hnov12 potassium channel"	
FT	FT	/note= "No stop codon given in specification"	
FT	FT	/transl_except= (pos:375, aa:Glu or Gly)	
FT	FT	/tag= b	
FT	FT	variation	
FT	FT	variation	
XX	PN	W09943696-A1.	
XX	PD	02-SEP-1999.	
PF	PF	22-FEB-1999; 99WO-US003826.	
XX			

PR	25-FEB-1998:	98US-0076687P.	
PR	07-AUG-1998:	98US-0095836P.	
PR	19-JAN-1999:	99US-0116448P.	
PA	(AXYS-) AXYS PHARM INC.		
XX			
PI	Miller AP, Curran ME, Hu P, Rutter M, Wang J;		
XX			
DR	WPI: 1999-527591/44.		
DR	P-PSDB; AA134123.		
PT	New nucleic acids encoding mammalian K-Hnov potassium channel proteins,		
PT	useful for the diagnosis and treatment of episodic ataxia with myokymia,		
PT	cardiac arrhythmia, epilepsy and Bartter's syndrome.		
PS	Claim 4; Page 57-60; 112pp; English.		
XX			
CC	This sequence represents human potassium channel K-Hnov12 cDNA. K-Hnov		
CC	proteins have a high degree of homology to known potassium channels and		
CC	may be alpha subunits, which form the functional channel, or accessory		
CC	subunits that act to modulate the channel activity. K-Hnov12 is a voltage		
CC	gated potassium channel. The gene's chromosomal location is Xp21.		
CC	determined via PCR chromosomal localisation using primers AA211926 and		
CC	AA211927. K-Hnov cDNAs were isolated by extension of expressed sequence		
CC	tags (ESTs) which were related but not identical to known human potassium		
CC	channels. Potential polymorphisms detected as sequence variants between		
CC	multiple independent clones. potassium channels have critical roles in		
CC	various cell types and biochemical pathways. Defective potassium channels		
CC	are known to cause four human diseases: episodic ataxia with myokymia;		
CC	cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.		
CC	As potassium channels are critical components of virtually all cells, it		
CC	is likely that abnormal potassium channels are also implicated in certain		
CC	renal, cardiovascular and central nervous system (CNS) disorders.		
CC	Nucleotides encoding K-Hnov proteins may be used for identifying		
CC	homologous or related proteins and the DNA sequences encoding them. They		
CC	may be used to produce compositions that modulate the expression and		
CC	function of the K-Hnov protein and in studying the biochemical pathways		
CC	associated with it. They may also be used for the recombinant production		
CC	of K-Hnov protein in fermentation cultures. Additionally, such		
CC	nucleotides may be used in gene therapy protocols for the treatment of		
CC	diseases associated with abnormal potassium channels		
XX			
SQ	Sequence 3424 BP; 680 A; 1081 C; 887 G; 775 T; 0 U; 1 Other;		
Alignment Scores:			
Pred. No.:	1,05e-170	Length:	3424
Score:	2123.50	Matches:	429
Percent Similarity:	76.93%	Conservative:	78
Best Local Similarity:	65.10%	Mismatches:	117
Query Match:	63.96%	Indels:	35
DB:	2	Gaps:	13
US-10-062-879-4 (1-636) x AA211901 (1-3424)			
QY	1 MetAlaAlaGlyValAlaAlaAlaTyrPheuProPheAlaArgAlaAlaAlaGlyTyrPMet	20	
Db	257 ATGGCGGACGGGCTGGCCACGGTGTCTTTTGTCTGGGACGACGAGGGGCTGGCTG	316	
QY	21 ProValAlaAsnCyseProMetuLapProAlaAspLysAenLysAaSGAlaSPGlu	40	
Db	317 CCCCAGGCGGACGACCCCTGTCCGCCCGGACCGGGGGGAGGAGGATCTCCAGAGATG	376	
QY	41 LeuIleValLeuAsnValserGIyArgrArpGheInThrTparGThrThrLeuGluArg	60	
Db	377 GTTCTGTGTGTGAAGTGAAGCGGAGCGGCTTTGAGATTGGAAGAAATACGCTGACGC	436	
QY	61 TyrProAspThrLeuLeuGlySerThrGluLysGluPhePhePheAsnGluAspThrLys	80	
Db	437 TACCCAGACACCTTGTGGGACGCTCGGAGAAAGGAAATCTTCACGATGCTGACTCAGC	496	
QY	81 GluTyrPhePheAspArgrAspProGluValPheArgCysValLeuAsnPheTyrArgThr	100	
Db	497 GAGAGACTTCTTGATCGACACCTTACATGTTCCGCCATGCTGGAACCTTACCGAAG	556	

QY	101	GLYIYSLEUHI	STR	PROARG	TYG	LU	CYS	I	LE	SER	AL	ATY	R	ASP	ASG	L	U	EN	L	A	PH	E	120	
			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
Db	557	GGGGGGCTGC	ATT	GGCCCA	CGG	CAG	AGT	GC	AT	CC	AGG	CTT	CG	AC	CA	GA	AG	CT	GG	CT	TT	C	616	
QY	121	TYRGLY	I	LEU	PRO	GL	I	LE	I	LE	I	LE	I	LE	I	LE	I	LE	I	LE	I	LE	140	
Db	617	TACGG	CC	TGG	TTC	CC	G	AG	CT	AG	T	CG	GT	AG	CT	CG	CT	CT	TA	GA	AG	AT	676	
QY	141	ARG	I	U	AN	A	GL	I	U	ARG	L	EU	ME	T	R	AS	P	AS	PN	A	S	ER	GI	160
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Db	677	AAGA	GA	AT	GC	CG	AG	CT	CG	CA	AG	AT	GA	GA	GG	CA	GA	GG	CA	GG	CA	GG	733	
QY	161	PRO	SER	LEU	-----	SER	PH	E	ARG	I	N	TH	ME	T	P	ARG	A	L	PH	E	GL	U	176	
			:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
Db	734	CCAG	CC	CT	CG	CA	G	AG	CA	G	AG	CT	CC	CT	GG	CA	G	CG	CT	CT	GG	CG	793	
QY	177	HIS	TR	SER	TH	LEU	A	LEU	V	A	L	P	HE	TYR	TYR	V	A	L	TH	GLY	P	HE	196	
Db	794	CAC	AC	G	AG	CA	CG	CA	G	CG	CT	CG	T	T	T	T	T	T	T	T	T	T	853	
QY	197	VAL	I	LE	TH	R	AN	A	GL	I	U	ARG	L	EU	TH	VAL	PRO	CYS	-----	GLY	TH	VAL	214	
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Db	854	GTC	AT	CC	CA	AT	GG	TA	GG	T	GA	GC	AT	CC	CA	AT	CG	CG	CG	CT	CG	CA	913	
QY	215	GLU	LEU	PRO	CYS	GLY	LU	ARG	TYR	SER	VAL	A	PH	PE	CYS	LU	ASP	TH	R	A	CYS	VAL	234	
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QY	235	MET	I	LE	PH	ETH	R	VAL	GLU	TYR	LEU	LEU	ARG	L	EU	PH	E	AL	A	PRO	SER	ARG	254	
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Db	974	CTC	AT	T	AT	T	CA	AG	GA	T	AT	CT	CT	CG	GG	CT	GG	T	T	T	T	T	1033	
QY	255	I	LE	ARG	SER	VAL	ME	SER	I	LE	ASP	VAL	A	LA	I	LE	ME	PRO	TYR	TYR	I	LE	274	
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Db	1034	CTG	CG	AG	AT	GC	AT	AG	CT	CG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	AT	CG	1093	
QY	275	VAL	ME	TH	R	AN	A	EN	GL	U	ASP	VAL	SER	GLY	A	PH	VAL	TH	LEU	ARG	VAL	PH	294	
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Db	1094	TTG	GT	GC	CA	AA	GA	AG	AT	GC	CT	CG	CG	CT	TT	GC	CA	CC	CT	CG	T	CG	1153	
QY	295	PH	E	ARG	I	LE	PH	Y	SER	PH	SER	ARG	HIS	ER	GIN	GLY	LEU	ARG	I	LEU	GLY	TH	314	
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OY		455	GluLeuThrGlyThrProGlnGlnGlnMet---GlyLeuThrThrsSerLeuIleGlu	473
			.....	
Db		1622	GAGACAGCGGCAGTGGGAGAAAGAGCTTTGTGTCAAGAACCCTTGCTTTGA	1681
OY		474	SerGlnHisHisLeuLeuHisCysLeuGlnLysThrThrsHisnHisgLuPheIleAsp	493
Db		1682	CAGCAACTATCCACTTGTCTGTCATGTCTTAGAAGAACAAAGTSCCATGAGTTCAAGAT	1741
OY		494	GluGlnMetPheGluGlnAsnCysMetGluSerSerMetGlnAsnTYrProSerThrArg	513
			:::	
Db		1742	GAGCTCACTTCAGTGA---GCCCTGAGAGCCCTCTCGCGGGGTGCGCACAGCCGT	1798
OY		514	SerProSerLeuSerSerHisPro-----GlyLeuThrThrsCysCysSer	529
			.....	
Db		1799	AGCACTCTGTGTCTTCCCACGACGAGGAGACCGGAAGCTGTCTTCTTGCTGCCCT	1858
OY		530	ArgArgSerLys---LysThrThrsIleuProHisSerAsnLeuProAlaThrArgLeu	548
Db		1859	CGCAGGGCCMAAGCCCGCGCATCCGCTTGCCCACTTCACAGTGCCTCAATGACGCCG	1915
OY		549	ArgSerMetGlnGluLeuSerThrIleHisIleGlnLysSerGlnProSerLeuThr	568
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Db		1916	GGCAGCATGACGAGCTGGACATG-----CTGGCAGAGGCTGGCAGAGCATGCCCT	1969
OY		569	ThrSerArgSerSerLeuAsnLeuAlaAspAspLYLeuArgProAsnCysLysThr	588
Db		1970	CAGAGCGCTCCACCTCAATGAGCCMACCCCCATACAGCTTGACTGAACCTGGACAGC	2029
OY		589	SerGlnIleThrThrAlaIleSerIleProThrProProAlaLeuThrProGluGly	608
Db		2030	CGGACATTGCTGCTGCATTAATAGATATCCCTACCTCTGCCAACACCCACAGAT--	2086
OY		609	GluSerArgProProProAlaSerProGly-----	618
			.....	
Db		2087	GAGAGCCA-----CCTCTCTCCCTCGGGCGGTGGCAGGCGCGGACAGCCTCAG	2140
OY		619	--ProAsnThrAsnIleProSerIleThrSerAsnValLysValSerValLeu	636
			:::	
Db		2141	AACCTCAGCCTGGGTACCCCTTGCTCTTCCCGCAGACTGTCAAGACTCATCCTGT	2197
<hr/>				
RESULT 20				
AAH99538				
ID	AAH99538	standard; cDNA; 2578 BP.		
XX	AC	AAH99538;		
XX	DT	16-OCT-2001 (first entry)		
XX	DE	Human protein encoding cDNA sequence SEQ ID NO:373.		
XX	KW	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;		
KM		antiflammatory; antirheumatic; antiarthritic; immunosuppressive;		
KM		antibacterial; endocrine; cardiac; central nervous system; vitruide;		
KM		anti-HIV; fungicide; antimutagen; cardiovascular; anemiaemic; anaemia;		
KM		antiggregant; haemostatic; vulnery; antifulcer; osteopathic; eczema;		
KM		dematological; antiallergic; antiasthmatic; antidiabetic; cystostatic;		
KM		neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;		
KM		immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;		
KM		antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;		
KM		cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;		
KM		genetic disease; hematopoietic disorder; platelet disorder; asthma;		
KM		chromocytopenia; osteoporosis; severe combined immunodeficiency;		
KM		allergic rhinitis; diabetes; multiple sclerosis; depression;		
KM		Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;		
XX		neurological disorder; ss.		
XX	OS	Homo sapiens.		
XX	PN	WO200153455-A2.		
PD	XX	26-JUL-2001.		
XX	PF	22-DEC-2000; 2000WO-USO35017.		



```
Qy 474 SerGlnHisHisLeuHisCysLeuGluLysThrThrAsnHisGluPheIleAsp 493
Db 1426 CAGCAATATCACCCTGCTGCTCACTGTCTAGAGAAAGACATGTCATGATTCACAGAT 1485
Qy 494 GluGlnMetPheGlnGlnAsnCysMetGluSerSerMetGlnAsnIYrProSerThrArg 513
Db 1486 GAGCTCACCTTCAGTGA--GCCCTGAGCCGCTCTGCCGGGTGGCCGACACAGCCGT 1542
Qy 514 SerProSerLeuSerSerHisPro-----GlyLeuThrThrThrCysCysSer 529
Db 1543 AGCACTCTGTGTCTCCAGCCAGTGGAGCCGGAAGCCGTGTCTTCTTGTGCTGCCCT 1602
Qy 530 ArgArgSerLys--LysThrThrHisLeuProAsnSerAsnLeuProAlaThrArgLeu 548
Db 1603 CGCAGGCCCAAGCCCGCCGATCCGCTTCCCAATCCA--CTGCCTCAGTCAAGCCGTG 1660
Qy 549 ArgSerMetGlnGlnLeuSerThrIleHisIleGlnGly--SerGlnGlnProSerLeu 567
Db 1661 GCAGGCATGCAGAGAGTGCACATG-----CTGGCAGGGCTTGGCAGAGACCATGCCCC 1714
Qy 568 ThrThrSerArgSerSerLeuAsnLeuLysAspArgLysLeuArgProAsnCysLys 587
Db 1715 TTCAGAGCCGCTCCAGCTTCAATGCCAAGCCCATGACAGCCTTGACTGAACTGCGAC 1774
Qy 588 Thr-SerGlnIleThrThrAlaIleIleSerIleProThrProProAlaLeuThrProG1 607
Db 1775 AGCGGGGAGACTTCGTGCTGCTGCTATTCAGCATCCCTTACCCTCTGCCAAGACCCAGA 1834
Qy 607 uGlyGluSerArgProProProAlaSerProG1Y----- 618
Db 1835 T--GAGAGCCAA-----CCTTCCTCCCTGGCGCGGTGGCAGGGCCGCGACACCCCT 1885
Qy 619 -----ProAsnThrAsnIleProSerIleThrSerAsnValIleValSerValIe 636
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Qy 636 u 636
Db 1946 G 1946
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QY 21 ProValAlaIaenCyseProMetProLeuAlaProAlaAspLysAsnLysArgGlnaAspGlu 40  
 DB 133 CCGGTGGCCCAACGCCCCCATGCCCCCTGGCCCCGCGCAAGAACAGCGCGAGATGAG 192  
 QY 41 LeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGluArg 60  
 DB 193 CTGATTCTCTCAACGAGAGTGGCGGAGGTTCACAGCTCGAGAGCAACGCTGGAGCCC 252  
 QY 61 TyrProAspThrLeuLeuGlySerThrGluLysGluPhePhePheAsnGluAspThrLys 80  
 DB 253 TACCCGAGACACCGCTGGCGAGACACGAGAAAGAGTTCTTCAACGAGACACCAAG 312  
 QY 81 GluThrPhePheAspAspAspProGluValPheArgCysValLeuAsnPheTyrArgThr 100  
 DB 313 GAGACTTCTTCAACGCGAGACCCGAGAGTGTCCGCTGCTCAACTTCAACGCGACG 372  
 QY 101 GlyLeuLeuHisThrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
 DB 373 GGGAGAGTGCACACCGCGCTACAGAGTGCATCTCTGCTACACAGACAGCTGGCTTC 432  
 QY 121 TyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArgLys 140  
 DB 433 TACGCGATCTCTCCGCGAGATCATCGGGGACTGCTGCTACGAGAGATCAAGACCGCAAG 492  
 QY 141 ArgGluAsnAlaGluArgLeuMetAspAspAspSerGluAsnAsnGlnGlnSerMet 160  
 DB 493 AGGAGAAACCGCGAGCTCATGAGACAGACAGACTCGAGAAACCAACGAGGTCAG 552  
 QY 161 ProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThrSerThr 180  
 DB 553 CCCTCGCTCAGCTTCCGCGACAGACCATGTGGCGGCTTCGAGAACCCCAACACACAGAG 612  
 QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
 DB 613 CTGGCCCTGGCTCTTCTACTACGAGACGAGCTGCTTCTTACGCTGCTCGGTCATCAACAA 672  
 QY 201 ValValGluThrValProCysGlyThrValProGlySerIleGluLeuProCysGlyGlu 220  
 DB 673 GTGGTGAAGAGCGGTGCGGACCGGTCCGCGACAGAAAGAGCTGCGCGGAGAG 732  
 QY 221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
 DB 733 CGCTACTCGGTGGCTTCTTCTGCTGAGACAGCGCGTGCATCATGATCTTCAACCGTGGAG 792  
 QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
 DB 793 TACCTCTGCGGCTCTTCCGCGCTCCAGCGCTACCGCTTCAATCCGACGTCATGAG 852  
 QY 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
 DB 853 ATCATCAACGTGGTGCATCATGCTTACTACATCGGTCTGTGTGATGACCAACCAAGAG 912  
 QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
 DB 913 GAGCTGTCGGCGCTTCTGTCAGCGCTCCGSGTCTTCCGATCTTCAAGATCTTCAAGTTT 972  
 QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320  
 DB 973 TCCCGCATTCCAGCGGCTGCGGATCTCGGCTACACACTGAAGAGCTGCTCCGAA 1032  
 QY 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThrValMetPhe 340  
 DB 1033 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092  
 QY 341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTyr 360  
 DB 1093 TATGCCAAGAAAGGCTCTCGCGCAAGATTCACAGATCCCTGCTGCTTGTGATC 1152  
 QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGly 380  
 DB 1153 ACATTTGTCAACATGACCACTGAGATACGAGAGATGTTGCTGAAGATTTGACAGG 1212  
 QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400

DB 1213 AAGATCTTGGCTCATCTGCTCTTGAAGTGGCTCTTGGTCACTTGGCTTCCAGTCCCT 1272  
 QY 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
 DB 1273 GTGATTGTTTCAACTTATAGCGGATTTTACCAACAGATCAAGAGCTGATTAACGACG 1332  
 QY 421 AlaglnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
 DB 1333 GCACAAAAGAGGCGCGCTTGGCAGAGATCCGTGTGGCCAAAAGAGCAGTTCAATGCA 1392  
 QY 441 TyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThrGlyThrPro 460  
 DB 1393 TACTGACACAGACCGCAACGAGCTCTTCAACAGAGCGCTGAGCTGACGGGACCCCA 1452  
 QY 461 GluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHisIleLeu 480  
 DB 1453 GAAGAGAGACATGAGGAGAACACCACTCATCTCATCGAGCGCAGATCATCACTGCTG 1512  
 QY 481 HisCysLeuGluLysThrThrAsnHisGluPheIleAspGluGlnMetPheGluGlnAsn 500  
 DB 1513 CACTGCTGGAAGAAACCACTAACCAAGATTTATGATGAGCAGATGTTGAGCAGAAC 1572  
 QY 501 CysMetGluSerSerMetGluAsnTyrProSerThrArgSerProSerLeuSerSerHis 520  
 DB 1573 TGCAATGAGATTTCAATGACAACTACCATTCACAAAGAGTCCCTCATCTGTCCAGCAC 1632  
 QY 521 ProGlyLeuThrThrThrCysCysSerArgArgSerLysThrThrHisIleuProAsn 540  
 DB 1633 CGAGGCTCATTAACACTGCTGCTCCGCTGTGTGAAGAAAGACACACACCTGCCAAT 1692  
 QY 541 SerAsnLeuProAlaThrArgLeuArgSerMetGlnLysSerThrIleHisIleGln 560  
 DB 1693 TCTAACCTGCACGCTACTCGCTCGCAGCATGCAAGAGCTCGACACAGATCCATCATCAG 1752  
 QY 561 GlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuValAlaAspAsp 580  
 DB 1753 GGCAGTGAAGACCCCTCCCTCAACAGTGTCTCAGCTTAAATTTGAAGACAGAGAC 1812  
 QY 581 GlyLeuArgProAsnCysLysThrSerGlnIleThrAlaIleIleSerIleProThr 600  
 DB 1813 GGAAGTGAACCAACTGCAAAACATCCAGATTCACACAGCATCATCAGATCCCACT 1872  
 QY 601 ProProAlaLeuThrProGluGlyGluSerArgProProAlaSerProGlyProAsn 620  
 DB 1873 CCCCCAGCGCTAACCCCGAGAGGGGAAAGTGGCCACCCCTGCGACGCCAGGCCCAAC 1932  
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 ; Sequence 1, Application US/09142791A  
 ; Patent No. 6368823  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Antoine Michel Alain Brill  
 ; APPLICANT: Thierry Paul Gerard Calmeis  
 ; APPLICANT: Jean-Francois Simon Pierre Faivre  
 ; APPLICANT: Jean-Luc Javre  
 ; APPLICANT: Sabine Rouane  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GH-30012  
 ; CURRENT FILING DATE: US/09/142, 791A  
 ; PRIOR FILING DATE: 1999-02-02  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
 ; PRIOR FILING DATE: 1998-03-23  
 ; PRIOR APPLICATION NUMBER: UK 9706377.0  
 ; PRIOR FILING DATE: 1997-03-27  
 ; PRIOR APPLICATION NUMBER: EP 97402971.2  
 ; PRIOR FILING DATE: 1997-12-09  
 ; PRIOR APPLICATION NUMBER: EP 97403007.4  
 ; PRIOR FILING DATE: 1997-12-11

NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 1  
; LENGTH: 2104  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-142-791A-1

Alignment Scores:

Score:	0	Length:	2104
Percent Similarity:	3311.00	Matches:	634
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Query Match:	99.73%	Mismatches:	2
		Indels:	0
		Gaps:	0

US-10-062-879-4 (1-636) x US-09-142-791A-1 (1-2104)

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21 ProValAlaAenCySPrometProLeuAlaProAlaAplysAsnLysArgGlnAspGlu 40  
61 CCGGTGGCCAACTGCCCATGCCCCCTGGCCCCGGCCCAAGAACAGCGGCAAGATGAG 120  
41 LeuIleValIleuAsnValSerGlyValArgPheGlnThrTrpArgThrThleuGluArg 60  
121 CTGATTGTCTTCAACGAGAGGGGGGAGGTTCCAGACTGAGAGCAACGCTGGAGGCG 180  
61 TyrProAspThrLeuLeuGlySerThrGlyLysGlyPhePheAsnGluAspThrLys 80  
181 TACCCGAGACCTCTGCTGGGAGCAAGAGAGAGTTCTTCTTCAACAGAGACACCGAG 240  
81 GluTrpPhePheAspArgAspProGluValAlaPheArgCysValIleuAsnPheTyrArgThr 100  
241 GAGTACTTCTTTCGACCCGGGAGCCCGAGGGTGTCCGCTGCTGCTCAACTTCTACCGCAG 300  
101 GlyLysLeuHisTyrTrpArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
301 GGGAGAGCTGACATACCCGCGCTACAGAGTCATCTGCTACGACGAGAGCTGGCTTC 360  
121 TyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArgLys 140  
361 TACGGCACTCTCCCGGAGATCATCGGGAGCTGCTGCTACGAGAGTACAGAACCGCAG 420  
141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnLysMet 160  
421 AGGGAGAACCGCGAGCGGCTCATGAGCAACGACTCGAGAACCAACCAAGAGTCCATG 480  
161 ProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThrSerThr 180  
481 CCCCTGCTCAGCTTCGCGACAGACATGCGGCGCTTCGAGAACCCCCACACACGACGCG 540  
181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
541 CTGGCCCTGGCTTCTACTACGTAAGCTGCTTCTTCACTGCTGCTGATACCAAC 600  
201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220  
601 GTGGTGGAGACGGTCCGCTGGCGACGGTCCCGGGAGCAAGAGAGTCCGCTGGGGAG 660  
221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
661 CGCTACTCGGTGGCTTCTTCTGCTGACAGCGGTGCTCATGATCTTACCGCTGAG 720  
241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
721 TACTCTCTGGGGCTCTTTCGGGCTCCAGCGGCTTCAACGCTTCAACCGAGGCTCATGAGC 780  
261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
781 ATCATGACGCTGGTGCATCATGCCCTTAACATCGGTGTGTCATGACCAACAGAG 840

281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
841 GACCTGTCCGGCGGCTTGTACAGCTCCGGGTCTTCCGGCTTCAAGATCTTCAAGTTT 900  
301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320  
901 TCCCGCACTCCAGGGCTGGGATCTGGGCTTACACACTGAAGAGCTGTGGCTCCGAA 960  
321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340  
961 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020  
341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTrpTyr 360  
1021 TATCCCGAAGAGGCTCTCTGGCCAGAGTTCACAGACNCTCTGCTGCTTTGGTAC 1080  
361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGly 380  
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381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
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401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
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1261 GCACAAAAGAGCGCGCTTGGCAGATCGTGTGGCCAAACAGGACAGTTGAAATGCA 1320  
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501 CysMetLeuSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSerSerHis 520  
1501 TGCATGAGAGTTCAATGAGAACTTACCATCCACAAAGAGTCCCTCATCTGCAGCCAC 1560  
521 ProGlyLeuThrThrThrCysSerArgArgSerLysThrThrHisLeuProAsn 540  
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1681 GGCAGTAGAGAGCCCTCTTCAACAGAGTCCCTCCAGCTTAAATTGAAGAAGCAGAGAC 1740  
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Db 1753 AACGCCAGCTACTCGCCTGGCAGCATGCAGACGATCCACATCCAGGCG 1812  
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Db 1873 CTGAGACCAAACTGCAAAACATCCAGATCAACAGCATCATCATGATCCCACTGCC 1932  
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Db 1933 CCACGCGTAAACCCAGAGGGGGAAGTCGGCCACCCCTGCCAGGCCCAACAGC 1992  
Qy 622 AsnIleProSerIleThrSerAsnValValLysValSerValLeu 636  
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; Sequence 3, Application US/09142791A  
; Patent No. 6368823  
; GENERAL INFORMATION:  
; APPLICANT: Antoine Michel Alain Bril  
; APPLICANT: Thierry Paul Gerard Calmejs  
; APPLICANT: Jean-Francois Simon Pierre Faivre  
; APPLICANT: Jean-Luc Javre  
; APPLICANT: Sabine Rouanet  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30012  
; CURRENT APPLICATION NUMBER: US/09/142, 791A  
; CURRENT FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: PCT/EP98/01901  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: UK 9706377.0  
; PRIOR FILING DATE: 1997-03-27  
; PRIOR APPLICATION NUMBER: EP 97402971.2  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: EP 97403007.4  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 2072  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
; US-09-142-791A-3  
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Score: 3291.50 Matches: 634  
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Best Local Similarity: 96.79% Mismatches: 2  
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Qy 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220  
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Qy      121 TYRGLYLEIUEUPROGLUILEIIEGLYASPCYSYTRGUGLUTYRLYASAPARGLYS 140
Db      617 TAGCGCTGCTGTTCCGAGCTAGTGTGATGCTGCTGCTGTAAGAGTATCGGAGCGAAG 676
Qy      141 ARGGLUANALAGIARGLEMETASPAAPASPSERGILUANANGLINGLUSERMET 160
Db      677 AAGGAGATGCCGAGCCCTGCGAGAGATGAGAGAGGAGGAGCGCGGAGACGCGC--- 733
Qy      161 PROSERIEU-----SERPHEARGLINHMETTPAPAGIALPHEGLUANPRO 176
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Qy      215 GLIUEUPROCYSGIYGLIUTYRTRYSERVALALAPHEPCYSEIHEIHSERVAL 234
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Qy      255 ILEARGSERVALMETSERILEIIEASPVVALALAIEMETPROTYRTRYILEGLYEU 274
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Qy      295 PHEARGIIEPHELYSPHESEARXHSERGINDIYLEUARGIIELEUGLYTRYTHLEU 314
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Qy      315 LYSERCYASLASERGIUEUGLYPHELEUUPHESELEUTHMETALAIIEILE 334
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Qy      335 PHEALATHRVALMETPHETRYALAGIULYSGYSESERIALASERLYSPHEHRSERILE 354
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Qy      355 PROALASERHETRPYRTRYTHRIIEVALTHMETHRHLEUGLYTRYGLYASPMETVAL 374
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Qy      375 PROLYSTRHRIIEAGIYLYSILEPHEGLYSERILECYSESERILEUSERGLYVALLEUVAL 394
Db      1394 CCGAGCAACATTTGCTGCGAAGATTTTCCGGTCCATCTGCTACATGAGGCTGTGTC 1453
Qy      395 ILEALAEUPROVALPROVALILEVALSERANPHESEARGLIETRYHISGLINANGLIN 414
Db      1454 ATTGCCCTGCTGTGCGACATGATGTGTCCAACTTATGCGCCCATCTACCAACCAACGAG 1513
Qy      415 ARGALAPLYSARGAGIAGIULYLYSIALAETHEUALAETGILAEYVALALAYS 434
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Db      1622 GAGGACAGCGGCACTGGCGAGAAACAGGCTTTGTGTCCAGAAACGTTCTGCTTGA 1681
Qy      474 SERGINIHSIHSIHSLEUENIHSYSELEUGIULYSTRHRSANHSIGIUPHEILEASP 493
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Qy      589 SERGINIETHRHALAIIEISERILEPROTHRPROALAEUTHRPROGLUGI 608
Db      2030 CGGACTCTGCGTGCATATATCAGATCCCTACCCCTGCGCAACCCAGAT--- 2086
Qy      609 GLUSERARGPROPROALASERPROGLY----- 618
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RESULT 8
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; Sequence 2456, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2456
; LENGTH: 3260
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2456

Alignment Scores:
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Query Match: 26.07% Indels: 13

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Db 931 GTGGCATCATCTTATTATTATCACTGGGTACCGAGTCCGCAAGCAGAGGGCAAT 990
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Qy 477 HisHisIleuLeuHisCysLeuGluIleThrThrAsnHisGluPheIleAspGluIleMet 496
Db 1516 TATATGGATCGAA-----GAGGGGGGTATGAACCATGACGCTTCCCGCACCCCT 1569
Qy 497 PheGlnGluAsnGlyMetGluSerSerMetGlnAsnTyTrProSerThrArgSerProSer 516
Db 1570 TTCAAAACGGGC-----AATTCACATCGCACCTCGCAC 1602
Qy 517 LeuSerSerHisProGly----- 522
Db 1603 ACGAAACATATCCCACTTGTGTCAACATCAAAAGATATTCACCGATGTTAATAT 1662
Qy 523 ---LeuThrThrThrCysCysSerArg 530
Db 1663 GTGATACAGTACATGCTGTGCTCAG 1689

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RESULT 10
US-09-949-016-12066
; Sequence 12066, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12066
; LENGTH: 7055
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12066

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## Alignment Scores:

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Pred. No.: 5,97e-63 Length: 7055
Score: 722.50 Matches: 175
Percent Similarity: 50.09% Conservative: 110
Best Local Similarity: 30.76% Mismatches: 175
Query Match: 21.76% Indels: 109
DB: Gaps: 16

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US-10-062-879-4 (1-636) x US-09-949-016-12066 (1-7055)

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Qy 18 GlyTrpMetProValAlaAsnCys-----PrometPro 28
Db 2142 GGGGCCCGGCTTCAAGCGCGGTGTGGCGGCGGCTGCGACCGCTACGAGCCGCTGCG 2201
Qy 29 -----LeuAlaProAlaAspIleAsnIleValAsnIleValIleValIleVal 46
Db 2202 CCTCATCTGCCGCGCGCGCGGCGGAGCAGACTCTGCGGGAGCCGCTGATCAATCAATC 2261
Qy 47 SerGlyArgArgPheGlnThrTrpArgThrThrLeuGluArgTyTrProAspThrLeuLeu 66
Db 2262 TCGGGGCGGCGCTTGCAGACGAGCTGAGAGCCCTTGGCCAGATGCCGAGAGCGCTGCTG 2321
Qy 67 GlySerThrGluIleGluPhe---PhePheAsnGluAspThrIleGlyTyTrPhePheAsp 85
Db 2322 GGCACCGCCCAAGCGCGCATGAGTACTTGCACCGCGTCCGCAAGATCTTCTTGCAC 2381
Qy 86 ArgAspProGluValPheArgCysValIleuAsnPheTyArgThr---GlyIleuHis 104
Db 2382 CGCAACCGCGCCAGCTTGCAGCGCATCTTCTACTACTATGATGTCGGGGCGCGATCCG 2441
Qy 105 TyrProArgTyArgIleCysIleSerAlaTyArgAspGluLeuAlaPheTyArgIleLeu 124
Db 2442 CGGCGGTCGAACGTCGCCATGACATTTCTCCGAGAGATCCGCTTCAACG----- 2495
Qy 125 ProGluIleIleGlyAspCysCysTyArgIleGluTyArgIleAspArgIleValAsnAla 144
Db 2496 -----CTGGGCGAGAGGCGCATGAGAAAGTTCCGCGAG----- 2528
Qy 145 GluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnIleuSerMetProSerLeuSer 164
Db 2529 -----GACGAGGCTTCTGCGGAGAGGAGGAGGCGCTTGCAGCGCGGAC 2576
Qy 165 PheArgGlnThrMetTrpArgAlaPheGluAsnProHisThrSerThrLeuAlaLeuVal 184
Db 2577 TTCCAGGCGCAGAGTGTGGCTGCTTGCAGTACCCGAGAGCTCCGGCGCGCGCGGCG 2636
Qy 185 PheTyTrValThrGlyPhePheIleAlaValSerValIleThrAsnValIleGluThr 204
Db 2637 ATCGCATCGTTCGCGGTGTCATCTCATCTTCTCATCTTCTGCTGCGAGACG 2696
Qy 205 ValProCysGlyThrValProGlySerIleGluLeuProCys----- 218
Db 2697 CTGCGG-----GAGTCCCGCAGAGAGAGATCCCGCTTCGACGTGCGAGACTCA 2750
Qy 219 -----GlyGluArg-----TyrSerVal 224

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Db 2751 TTGAGACGACCGGCAACAGACGTGGGGTCCCGGCGAGACCTCCAGCTTCTCCGAT 2810  
 Qy 225 AlaphetheCysleuapthralaCysValMetilePheTherValgluTyrluLeuarg 244  
 Db 2811 CCTCTTCTGCTGGTGGAGACGTGTCATCATCTGGTTCCTTCGAAACGTGGTGGCG 2870  
 Qy 245 LeuphelelalaProserargTyrrargPhelelaxSerValMetSerlellelAapVal 264  
 Db 2871 TTCTTGGCTTGTCTGACCAAGCCACTTCTCGGAAACATCAATGACCTGACATT 2930  
 Qy 265 ValAlaileMetProTyrrTyrlleGllyLeuValMet-----Thr 277  
 Db 2931 GTGGCCATCATCTCTTATTATTAACACTCTGGTAACGAGCTGGCGAAGACGCGCAT 2990  
 Qy 278 AsnAsnGluAspValSerGlyAlaPheVal---ThrleuArgValPheArgValPheArg 296  
 Db 2991 GACAGACGCGCATGCTCTGGCCATCTGAGGGTCACTCCGCTGGTAAGCTTCCCGC 3050  
 Qy 297 IlePheIysPheSerArgHisSerGlnGlyLeuArgGlyleuGlyTyrrThrleuIysSer 316  
 Db 3051 ATCTTCAAGCTGTGCGCCCACTCCAGGGGCTGACAGTCTCGGCAACGCTGAAGGCG 3110  
 Qy 317 CysAlaSerGluLeuGlyPheLeuLeuPheSerleuTherAlaIlellelelPheAla 336  
 Db 3111 TCCATGGGAGAGCTGGGATTCATCTTCTCTTATTGGGGCATCTTCTTCTC 3170  
 Qy 337 ThrValMetPheTyrrAlaGluTyrglySerSerAlaSerIysPheTherSerleProAla 356  
 Db 3171 AGCCGCGTCACTTTCGCGAGGACAGACCCCACTTCAGGTTTCAGCAGCATCCCGCAT 3230  
 Qy 357 SerPheThrTyrrThrIleValThrMetThrThrleuGlyTyrrGlyAspMetValProIys 376  
 Db 3231 GCCTTCTGTGGGAGAGTGGTACCATGACCAAGTGGTTACGCGATATGACCCAGTGG 3290  
 Qy 377 ThrIleAlaGlyIysIlePheGlySerIleCysSerleuSerGlyValleuValIleAla 396  
 Db 3291 ACCATAGGCGGCAAGATTTGGGATCTCTGTGCCATCCCGGTGCTTGGACATCGCA 3350  
 Qy 397 LeuProValProValIleValSerAsnPheSerArgIleTyrrHisGlnAsnGlnArgAla 416  
 Db 3351 TTGGCAGTTCCTCGGATTTGTTCCAACTTCACTTACCACTTCGAGGAGACAGAAAGG 3410  
 Qy 417 AspIysArgArgAlaGlnIlyblybAlaArgleuAlaArgIleArgValAlaIlybThrGly 436  
 Db 3411 GAAGAGCA----- 3419  
 Qy 437 SerSerAsnAlaTyrlleuHisSerIysArgAsnGlyleuLeuAsnGlnAlaIleuGluLeu 456  
 Db 3420 -----TCCAGTACATGCAC-----GTGGAACTTCCGACACCTC 3455  
 Qy 457 ThrGlyThrProGluGluGluIleMetGlyIysThrThrSerleuIleGluIysGlnHis 476  
 Db 3456 TCCCTTTCAGCCGAGGAGCTCCGAAAGCAAGAGTAACTGACCTGAGTAAGTGGAG 3515  
 Qy 477 HisIleIleuIleHisCysleuGluIlyblybThrThrAsnHisgluIlelelAapGluIleMet 496  
 Db 3516 TATATGGTGTATCGAA-----GAGGGGGTATGAAACATGACGCTTCCCGACGACCTC 3569  
 Qy 497 PheGluGluIleAsnGlyMetGluSerSerMetGlnAsnTyrrProSerThrArgSerProSer 516  
 Db 3570 TTCAAAACGGGC-----AATTTCACCTGCGACCTGCAC 3602  
 Qy 517 LeuSerSerHisProGly----- 522  
 Db 3603 ACAGAACATATATCCCACTGTGTGTCACATCAAAAAGATATTCACCGATGTTAATAT 3662  
 Qy 523 ---LeuThrThrThrCysCysSerArg 530  
 Db 3663 GTGATACAAAGTACATGCTGTGTACG 3689

RESULT 11  
 US-09-949-016-14035  
 ; Sequence 14035, Application US/09949016

; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH TYPE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; PRIORITY FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 14035  
 ; LENGTH: 7056  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-14035  
 Alignment Scores:  
 Pred. No.: 5,97e-63 Length: 7056  
 Score: 722.50 Matches: 175  
 Percent Similarity: 50.09% Mismatches: 110  
 Best Local Similarity: 50.76% Indels: 109  
 Query Match: 21.76% Gaps: 16  
 DB: 4  
 US-10-062-879-4 (1-636) x US-09-949-016-14035 (1-7056)  
 Qy 18 GlyTrpMetProValAlaAsnCys-----PromerPro 28  
 Db 2142 GGGGCCCCGCTCAAGGCGGCTGTGGCGGCGCGCTGCGACCGCTACGAGCGCTGCGC 2201  
 Qy 29 -----LeuAlaProAlaAspIysAsnIlyblybArgGlnAsnGluIleValleuAsnVal 46  
 Db 2202 CCTTCATCGCGCGCGCGCGGAGACAGACTGCTGCGGAGCGCGGTGATATACATC 2261  
 Qy 47 SerGlyArgAspPheGlnThrThrPArgThrThrleuGluArgTyrrProAspThrleuLeu 66  
 Db 2262 TCCGGGCTGCCCTTGCAGACCACTGAAAGCCTTTGGCCAGTTCCTCCGAGACCTGCTG 2321  
 Qy 67 GlySerThrGluIlyblybPhe-----PhePheAsnGluAspThrIlybGlyTyrrPhePheAsp 85  
 Db 2322 GCGCAGCCCAAGCGCGCGCATGAGTACTTGCAGCCGCTCCGACAGAGTACTTCTGAC 2381  
 Qy 86 ArgAspProGluValPheArgCysValleuAsnPheTyrrArgThr-----GlyIysleuHis 104  
 Db 2382 CCGAACCGGCGCGAGCTTGCAGCGCATCTTACTATCACTGATCGGCGCGCGCATCCG 2441  
 Qy 105 TyrProArgTyrrGluCysIleSerAlaTyrrAspAsnGluIleAlaPheTyrrGlyIleleu 124  
 Db 2442 CGGCGGTCMAAGTCCCATGACATTTCTCCAGAGAGATCCGCTTACAG----- 2495  
 Qy 125 ProGluIleIleGlyAspCysCysTyrrGluIlyblybAspArgIysArgGluAsnAla 144  
 Db 2496 -----CTGGGAGAGAGCGCATGAGAAATTCCGCGAG----- 2528  
 Qy 145 GluArgleuMetAspAspAsnAspSerGluAsnAsnGlnGluIysMetProSerleuSer 164  
 Db 2529 -----GACGAGGCTTCTCGCGGAGAGAGCGCGCTTCCCGCGGAC 2576  
 Qy 165 PheArgGlnThrMetTyrrArgAlaPheGluAsnProHisThrSerThrleuAlaIleuVal 184  
 Db 2577 TTCCAGCGCGAGTGTGCTCTTTCAGATGACCCCGAGACTCCGGCGCGCGCGGCGC 2636  
 Qy 185 PheTyrrTyrrAlaThnglyPhePheIleAlaValSerValIleThrAsnValAlaGluThr 204  
 Db 2637 ATCGCCATGATGTGCTGCTGTGATCTTCATTCATTCATTCATTCATTCATTCATTCAT 2696  
 Qy 205 ValProCysGlyThrValProGlySerIysgluLeuProCys----- 218

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Db      2697 CTGCG-----GAGTTCGGACGAGAAAGACTAACCCGCTCGACGTCCGAGACTCA 2750
Qy      219 -----GlyAluArg-----TyrSerVal 224
Db      2751 TTCGAGACGACGGCGAACGACGCTCGGGGTCGCCGCGAGAGACCTCAGCTCCCAT 2810
Qy      225 AlaphPheCysLeuAapThrAlaCysValMetIlePheThrValGluTyrLeuLeuArg 244
Db      2811 CCCTTCTTCGTCGTCGAGACCTGTCATCATCTGTTCTCTTCGACATGCTGGTGGCG 2870
Qy      245 LeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSerIleIleAspVal 264
Db      2871 TTCTTCGCTGCTCTAGCAAAAGCCACTTCGCGAAACATCATGACCTGATGACATT 2930
Qy      265 ValAlaIleMetProTyrTyrIleGlyLeuValMet-----Thr 277
Db      2931 GTGGCCATCATCTCTTATTTATCATCTCGGGTACCGAGCTGGCCGAAAGACGGCAAT 2990
Qy      278 AsnAsnGluAapValSerGlyAlaPheVal---ThrLeuArgValPheArgValPheArg 296
Db      2991 GGACAGACGACGACGATCTCTGCGCATCTGAGGGTCATCCGCTGGTAAAGGCTCTCCGC 3050
Qy      297 IlePheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSer 316
Db      3051 ATCTTCAAGCTGTGCGCCCACTCCAGAGGGCTGACAGATCTCCGGCAAAACCTGAAAGCG 3110
Qy      317 CysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAla 336
Db      3111 TCATCGGGGAGTGGAGTGTCTCATCTTCTCTTATTTGGGGTCACTCTTTCTCC 3170
Qy      337 ThrValMetPheTyrAlaGluLeuGlySerSerAlaSerLysPheThrSerIleProAla 356
Db      3171 AGCGCGGTCTACTTGTCCGACGACGACGCCCACTTCAAGATTTCACGACGATCCCGCAT 3230
Qy      357 SerPheTyrTyrThrIleValIleValIleThrMetThrThrLeuGlyTyrGlyAspMetValProLys 376
Db      3231 GCCTTCTGTCGGACGTCGACGTCATGACACAGCGGTTACGCGAATATGACCCCATG 3290
Qy      377 ThrIleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAla 396
Db      3291 ACCATAGGGGGCAGAGATGTGGAGTCTCTGTGTCATCGCGGGTCTTACCATCGCA 3350
Qy      397 LeuProAlaProValIleValIleSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAla 416
Db      3351 TTGCGAGTCCCGGATTTGTTTCCAACTTCAATTACTTTCACACCGGAGACAGAAAGG 3410
Qy      417 AspLysArgAlaGlnIleLysAlaIleArgLeuAlaArgIleArgValAlaLysThrGly 436
Db      3411 GAAGAGCA----- 3419
Qy      437 SerSerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGluAlaLeuGluLeu 456
Db      3420 -----TCCAGTATCATGCAC-----GTGGGAAGTTGCGACAGACTC 3455
Qy      457 ThrGlyThrProGluGluGlnHisMetGlySerThrThrSerIleGluSerGlnHis 476
Db      3456 TCCCTTCTCAGCGGAGGCTCCGAAAGCAAGATACCTGACCTGAGTAAGTCGAG 3515
Qy      477 HisIleLeuLeuHisCysLeuGluLysThrThrAsnHisGluPheIleAspGluMet 496
Db      3516 TATATGCGATCGAA-----GAGGGGGGTATGAAACCATAGCGCTTCCCAAGACCCCT 3569
Qy      497 PheGluGlnAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSer 516
Db      3570 TTCAAAACGGGCG-----AATTCACATGCGACACTGCGAC 3602
Qy      517 LeuSerSerHisProGly----- 522
Db      3603 ACGAACATATATCCCACTTGTGTCAACATCAAAAAGATATTTCACCGATTTAATAT 3662
Qy      523 ---LeuThrThrTyrCysCysSerArg 530

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Db      3663 GTGATACAGTACATGCTGTGCTCAG 3689
RESULT 12
US-09-949-016-324
; Sequence 324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-324

Alignment Scores:
Pred. No.: 1,73e-63 Length: 3004
Score: 721.50 Matches: 175
Percent Similarity: 50.09% Conservative: 110
Best Local Similarity: 30.76% Mismatches: 175
Query Match: 21.73% Indels: 109
DB: Gaps: 16

US-10-062-879-4 (1-636) x US-09-949-016-324 (1-3004)
Qy      18 GlyTyrMetProValAlaAsnCys-----PromerPro 28
Db      138 GGGGCCCCGCTCAAGCGGCTGTGGCGGGCGGCTGCCACCGCTACGAGCGGCTCCG 197
Qy      29 -----LeuAlaProAlaAspLysAsnLysArgGlnAspGluLeuIleValLeuAsnVal 46
Db      198 CCTCATCTGCGCGCGCGGCGGAGACGACGTGCTGGGAGGCGCGGTATCATCATC 257
Qy      47 SerGlyArgArgPheGlnThrTyrPargThrThrLeuGluArgTyrProAspThrLeuLeu 66
Db      258 TCCGCGCTGCGCTTCGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 317
Qy      67 GlySerThrGluLysGluPhe-----PhePheAsnGluAspThrLysGluTyrPhePheAsp 85
Db      318 GGGCACCACCAAGCGGCGCATGAGTACTTGCACCCGCTCCGCAACGATCTTCTGCAC 377
Qy      86 ArgAspProGluValPheArgCysValLeuAsnPheTyrArgThr---GlyLysLeuHis 104
Db      378 CGCAACCGGCGCCAGCTTCAAGCCATCTTACTACTATGATGATCGGGGCGGATCGC 437
Qy      105 TyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPheTyrGlyIleLeu 124
Db      438 CGGCGGCTCAACGTCGCCATTCGACATTTCTCCGAGGAGATCGGCTTCTACAG----- 491
Qy      125 ProGluIleIleGlyAspCysCysTyrGluGluTyrIleAspArgLysArgGluAsnAla 144
Db      492 -----CTGGCGGAGGAGCCATGAGAAAGTCCGCGAG----- 524
Qy      145 GluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnLysSerMetProSerLeuSer 164
Db      525 -----GACGAGGCTTCTCGCGGAGGAGAGAGAGGCGCTTCCCGCGGAC 572
Qy      165 PheArgGlnThrMetTyrPargAlaPheGluAsnProHisThrSerThrLeuAlaLeuVal 184
Db      573 TTCGAGCGCAGAGTGTGCTGCTTTCGACTACCCGAGAGCTCCGGGCGGCGCGGCGGCG 632

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Qy 185 PheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsnValValGluThr 204
Db 633 ATGCCATCGTGTCCGTCGTGATCTCATCTCATCTTCCTGCTGGAGAGC 692
Qy 205 ValProCysGlyThrValProGlySerGlyLeuProCys----- 218
Db 693 CTGCG-----GAGTTCGGCGAGAGAGACCTACCCGCTCGACGTGACGACTCA 746
Qy 219 -----GlyGluArg-----TyrSerVal 224
Db 747 TTCGAGCAGCCGCGCAACAGCAGTCGCGGTCCGCGAGAGCCTTCAGCTTCGAGT 806
Qy 225 AlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGluTyrLeuLeuArg 244
Db 807 CCTCTTCTGTCGTGGAGACGCTGTGCATCATCTGCTCTTCCTTCAGACTGTGTGGC 866
Qy 245 LeuPheAlaIaProSerArgTyrArgPheIleArgSerValMetSerIleIleAspVal 264
Db 867 TTCTTCGCTGTCTACCAAGCACCTTCGCGAACAATCATGAACTGATCGACATT 926
Qy 265 ValAlaIleMetProTyrTyrIleGlyLeuValMet-----Thr 277
Db 927 GTGCGCATCATCTCTATTATTATCACTGTGTAACGAGTGGCCGACAGACGAGGCAAT 986
Qy 278 AsnAsnGluAspValSerGlyAlaPheVal-----ThrLeuArgValPheArgVal 296
Db 987 GAGACGAGCGCATGTCTGCGCATCTGAGGAGTCACTGCGGTGAGGGCTTTCGCG 1046
Qy 297 IlePheIlePheSerArgIleSerGlnGlyLeuArgIleLeuGlyTyrThrLeuIleSer 316
Db 1047 ATCTTCAAGCTGTGCGCCACTCCAGAGGGCTGAGATCTCGGGGCAAAAGCTGAAAGGG 1106
Qy 317 CysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAla 336
Db 1107 TCCATGCGGAGCGGATGCTCATCTCTCTCTTTATGAGGAGCATCTTCTCTCC 1166
Qy 337 ThrValMetPheTyrIleGluIleGlySerSerAlaSerIlePheThrSerIleProAla 356
Db 1167 AGCGCGGTCTACTTGGCGAGGAGCAGACCCCACTTCAGGTTTCAGACCATCTCCGAT 1226
Qy 357 SerPheTyrTyrThrIleValIleThrMetThrThrLeuGlyTyrGlyAspMetValProIys 376
Db 1227 GCCTTCTGTGGAGAGGTACCATGATCAACAAGCTGATACCGCATATGACCCAGT 1286
Qy 377 ThrIleAlaGlyIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAla 396
Db 1287 ACCATAGGGGAGCAAGATTGAGGATCTCTGTGCCATCCCGGTGCTTGACCATGCA 1346
Qy 397 LeuProAlaProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAla 416
Db 1347 TTGCCAGTTCCTCGATGTTTTCACACTTCACTTCAACACCGGAGACAGAAAGG 1406
Qy 417 AspIleAspArgAlaGlnIleIleAlaArgLeuAlaArgIleArgValAlaIleIleThrGly 436
Db 1407 GAAAGACAA----- 1415
Qy 437 SerSerAsnAlaTyrLeuHisSerLeuIleArgAsnGlyLeuLeuAsnGluAlaLeuGluLeu 456
Db 1416 -----TCCAGTACATGCAC-----GTGGGAAGTTCCAGACACTC 1451
Qy 457 ThrGlyThrProGluGluGluHisMetClyIleThrThrSerLeuIleGluSerGlnHis 476
Db 1452 TCCCTTTCAGCCGAGAGCTCCGAAAGCAAGCAAGTCACTCGAGTAAAGTCGAG 1511
Qy 477 HisIleLeuLeuHisCysLeuGluIleThrThrAsnHisGluPheIleArgGluGlnMet 496
Db 1512 TATATGTGATCGAA-----GAGGGGGATATGACATAGCGTTTCCCGACAGACCC 1565
Qy 497 PheGluGlnAsnGlyMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSer 516
Db 1566 TTCAAAACGGGC-----AATTCACCTGCACCTGACAC 1598
Qy 517 LeuSerSerHisProGly----- 522

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Db 1599 ACGAACAATATATCCCACTGTGTGTCACATCAAAAGATATTCACCGATGTTATAT 1658
Qy 523 ---LeuThrThrThrCysCysSerArg 530
Db 1659 GTGATACAAAGTACATGCTGTGTCTGAC 1685

RESULT 13
US-07-955-916-6
/ Sequence 6, Application US/07955916
/ Patent No. 5397702
/ GENERAL INFORMATION:
/ APPLICANT: CAHALAN, Michael D.
/ APPLICANT: CHANDY, Kantanchara G.
/ APPLICANT: KRISMER, Stephen
/ APPLICANT: GHANSHANI, Sanjiv
/ APPLICANT: GUTMAN, George A.
/ APPLICANT: DETHLEFS, Brent A.
/ TITLE OF INVENTION: ASSAY FOR AND TREATMENT OF AUTOIMMUNE
/ DISEASES
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Walter H. Dreyer
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/955,916
/ FILING DATE: 19921002
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dreyer, Walter H.
/ REGISTRATION NUMBER: 24,190
/ REFERENCE/DOCKET NUMBER: A-54474-3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1805 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-07-955-916-6

Alignment Scores:
Pred. No.: 4,24e-63 Length: 1805
Score: 714.00 Matches: 195
Percent Similarity: 46.05% Conserved: 91
Best Local Similarity: 31.40% Mismatches: 183
Query Match: 21.51% Indels: 152
DB: 1 Gaps: 20

US-10-062-879-4 (1-636) x US-07-955-916-6 (1-1805)

Qy 20 MetProValAlaAsnCysProMetProLeuAla-----Pro 31
Db 74 CTCCTCCCTGAGGAGGAGCTCCATGGGTGTGCTGGGCGCGCATGCTAAGGGGGCGCC 133
Qy 32 AlaAspIleAsnIleAspGlnAspGluLeuIleValLeuAsnValSerGlyArgArgPhe 51
Db 134 GCGATGGCCCAAGGGGAGAGGAGCGGATCGTGTATCAACGTGGGCGGACCGCGCAC 193
Qy 52 GlnThrTyrArgThrThrLeuGluIleArgTyrProAspThrLeuLeuGly----- 67

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Qy      499  GlnAsnCyseMetGluSerMetGlnAsnTyProSerThrArgSerProSerLeuSer 518
      1608  GAGGGGGGTATGAACAGAGGCC-----TTCCCGAGAGACCCCTTCAAAACGGGCAAC 1661
Qy      519  SerHisProGlyLeuThrThrThrCysCysSerArgArgSerLysLysThrHisLeu 538
      1662  TCC-----ACAGCACTTGC-----ACCACGACAAATTAAC 1691
Qy      539  ProAsnSer 541
      1692  CCCAACTCC 1700

RESULT 15
US-09-949-016-1250
; Sequence 1250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1250
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1250

Alignment Scores:
Pred. No.:      2,05e-62      Length:      3186
Score:          711.50      Matches:      213
Percent Similarity: 40.69%      Conservative: 106
Best Local Similarity: 27.17%      Mismatches:   233
Query Match:    21.43%      Indels:       232
DB:              4          Gaps:         23

US-10-062-879-4 (1-636) x US-09-949-016-1250 (1-3186)
Qy      23  AlaAsnCyseProMetProLeuAlaProAlaAspLysAsnLysArg----- 37
      461  GCGGGCCCCCGGACCCCGGCGCGCGGAGACCGGCGCGGAGCCATGCCCGGGCTG 520
Qy      38  -----GlnAspGluLeuLysValLeu 44
      521  CCGGGCGGCGGCATGGGGCGGACAGCGCGCGGCTGGCGACAGCGGCAAGATCGTATC 580
Qy      45  AsnValSerGlyArgGlyPheGlnThrThrArgThrThrLeuGluArgTyProAspThr 64
      581  AACCTGGCGCGCGCTGGCATGAGACGATCCGCTGACGCTGCCACCCCTGCCGGGAGC 640
Qy      65  ---LeuLeuGlySerThrGluLysGlu-----PhePhePheAsnGluAspThr 79
      641  CCGCTGGCGCGCGCTGACGAGACCCGAGCGCGGCGGCGGCGCTTGCATGACTAGACCCGGGCGCC 700
Qy      80  LysGluTyRhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyArg 99
      701  GACGAGTTCTTCTTGAACCGGACACCGGGAGTCTTCGCGTACGTCACACTACTACCGC 760
Qy      100  ThrGlyLysLeuHisTyRProArgTyRGlucysLieserAlaTyRAspAspGluLeuAla 119
      761  ACCGGCAAGCTGCACTGCGCCAGCGACGCTGGCGGGCCCTGTTTGGAGAGAGACTCGGC 820
Qy      120  PheTyRglyLeuProGluLysLeuLysAspCysTyRGlucLysTyRAspArg 139

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Db      821  TTCTGGGGCATTCACAGACCGACCGAGCGCTGCTGATGACTTAC-----CGG 874
Qy      140  LysArgGluAsnAlaGluArgLysMetAspAsp----- 150
      875  CAGATCGCAGCGCTGAGAGAGCGCTGACTCTTTCAGAGCGCCCAACCCCGGGGCGCC 934
Qy      151  -----AsnAspSerGluAsnAsnGlnGluSer----- 159
      935  GCCAAGCGCGCAACCGCCGAGCGCCACAGACGAGCGCTGAGACGAGCGGCGCG 994
Qy      160  -----MetProSerLeuSerPheArgGlnThr 168
      995  GCGCGCGCGCGCTGACGAGCGCGCGGAGCTCAAGCGCTTGCCTTCAGAGCGC 1054
Qy      168  ----- 168
      1055  GCGCGCGCGCGCGCGCGCGCGCCAGCGGCGCGCGCGCGCGCGGCGGACATGCTGCGC 1114
Qy      169  -----MetTrpArgAlaPheGluAsnProHisThrSerThrLeuAlaLeu 183
      1115  CGCTGGCAGCCCGCGGTGTGGGCGCTTTCAGAGACCCCTTACGTGCGGGCGCGCAGG 1174
Qy      184  ValPheTyRtyrValThrGlyPhePheLeuValSerValLethAsnValValGlu 203
      1175  TATGTGGCTTCGCGCTCCCTCTTCTTCATCTCATCTTCATCAACACCTTCTGCTGAA 1234
Qy      204  Thr-----ValProCysGlyThrValProGlySerLysGluLeuPro 217
      1235  ACCCATGAGGCGCTTCATCATATTAGACAAAGACGCTGACCCAGCGCTCCGATCCC 1294
Qy      218  CysGlyValArgTyRSerValAlaPhePheCysLeuAspThr----- 231
      1295  GGGGACCTCCGAGAACATCACCAAGTGAAGTGAAGACGCCCTTCTGACCTAC 1354
Qy      232  -----AlaCysValMetLeuPheThrValGluTyRLeuLeuArgLysPheAla 248
      1355  GTGAGAGGGGTGTGGCGGTGTGCTGTTCACTTCGAGTCTTCATGCGCATCACTTCTGC 1414
Qy      249  ProSerArgTyRArgPheLeuArgSerValMetSerLeuLethAsnValAlaLeuMet 268
      1415  CCAGACACGTGAGATTCTTAAAGACGCTTCAACATCTGATGATGTCGCGCATCTG 1474
Qy      269  ProTyRtyrLeu-----GlyLeuValMetThrAsnAsnGluAspValSer 283
      1475  CCTTCTATCTCGAGGTGGGCGCTCTCGGCTCAGCTCCAGAGCGCGCAAGAGTCTG 1534
Qy      284  GlyAlaPheValThrLeuArgValPheArgValPheArgLysPheSerArgHis 303
      1535  GCGTTCGTGGGGGTGTGCGCTTCTGCGCATCTGCGCATCTTCAAGTGAAGTCCGCGAC 1594
Qy      304  SerGlnGlyLeuArgLysGlyTyRThrLeuLysSerCysAlaSerGluLeuGlyPhe 323
      1595  TTGCTGGGCTGGCGCGTGGGACACACGCTCCGCGCAGCAACCAAGTCTGCTG 1654
Qy      324  LeuLeuPheSerLeuThrMetAlaLeuLeuPheAlaThrValMetPheTyRAlaGlu 343
      1655  CTCATCATCTTCTTCTGCGCTGGGGGTCTCATCTTGCACACATGATTTACTAGCTGAG 1714
Qy      344  Lys-----GlySerSerAlaSerLysPheThrSerLeu 354
      1715  CGCATTTGGCGCGACCCCGATGACATCTGGGCTCAACACACATCTTCAAGAACATC 1774
Qy      355  ProAlaSerPheTyRtyrThrLeuValThrMetThrThrLeuGlyTyRgluAspMetVal 374
      1775  CCATTCGCTTCTGTGTGGGTGTGTCACATACAGACCTCGGCTATGAGACATGTAC 1834
Qy      375  ProLysThrLethAlaGlyLysLysPheGlySerLysCysSerLeuSerGlyValLeuVal 394
      1835  CCGAAGACGTGTGCGGAGATGCTGTGCGGGCGCTGTGTCTCTGCGGGGGGTGTGACC 1894
Qy      395  LethAlaLeuProValProValLethValSerAsnPheSerArgLysGlnAsnGln 414

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Db      1895 ATGCCATGCTGTGCCCCGCTCATTTGTCAACAACACTTTGGCATGTACTATTTCGTGGCCATG 1954
Qy      415 ArgAlaAspIysArgArgAlaGlnIlyValIaArgLeuAlaArg----- 429
Db      1955 GCCAAGCAGAAGCTGCGCCAAAGAAAGAACAAACATATCCCCGGCCCCCGCAACCGGGC 2014
Qy      429 ----- 429
Db      2015 TCGCCCACTACTGTCAAGCTGCAACCCACCCCGCCACCCCGCCCAACCCGCAACCGGC 2074
Qy      430 -----1leatValAla 433
Db      2075 AGCGGGGGCATCAGCCCCCGCCACCCATCATCCCACTTCATGGGGGGTGAATGTGGCC 2134
Qy      434 LysThrGlySerSerAsnAlaYrLeuHisSerIysArgAsnGlyLeuAsn----- 451
Db      2135 GGGGCTTACCACGAGGGGGCCCAACAGCACGCC-----GGGCTGTCTCAGGGGGGGA 2185
Qy      452 ---GluAlaLeuGlnLeuThrGlyThrProGluGluGlnHisMetGlyIysThrThrSer 470
Db      2186 GCGGGTGGGTGGGATCATGGGGCTGCTCTCTGCGCAAGCCCCGCGAGCTTGGCCG 2245
Qy      471 LeuIleGluSerGlnHisHisIleLeuLeuHisCysLeuGlnIlyThrThrAsnHisGlu 490
Db      2246 TTGGCTCAG----- 2254
Qy      491 PheIleAspGluGlnMetPheGluGlnAsnCysMetGluSerSerMetGlnAsnYrPro 510
Db      2255 -----GAGGAGGTGATTGATGATCAACCGGGGAGATCTCGCCCAATGGGGATCCG 2305
Qy      511 SerThrArgSerProSerIleuSerSerHisProGly-LeuThrThrThrCysSerArg 530
Db      2306 GCGACAGCTCGCTTGGCCACGAGAGACTGCCACCATTTACACAGCTGCGCATGTGCCG 2365
Qy      530 GATSerIlyLeuThrThrHisIleu----- 540
Db      2366 GAGACACAGAGCCCCCATCAAGCCTGTGAAGACCTGGCCGCTATAGCCGGACCGAGCTCCG 2425
Qy      540 nSerAsnLeuProAlaThrArgLeuArgSerMetGlnIleuSerThrIleHisIleG 560
Db      2426 TTCTCTCTCAACCGACTATGCCCCCTT----- 2450
Qy      560 nGlySerGluGlnProSerIleuThrThrSerArgSerSerLeuAsnLeuIlyAspAs 580
Db      2451 -----CCCTGATGCTCTCCATCCGAAAGCCACTGTGCTC----- 2486
Qy      580 pGlyLeuArgProAsnCys-----LysThr-----SerGlnIleThrAlaIle-- 595
Db      2487 -----CCCACTGCCCCCCCCCAAGACTGGCGTGAAGCCAGGCCCCCCCAAGCTTCTG 2536
Qy      596 ---IleSerIleProThrPro--ProAlaLeuThrProGluGlyGluSerArgProFr 613
Db      2537 CCGGACTCAAGCGCAAGCGCGGGCTGTGATATCCCTTAGAGCAAGACCCCTCCCC 2596
Qy      613 O-----ProAlaSerProGlyPr 619
Db      2597 CCGGGCTTGTGTACCGCCTGAGACCTCGGAGAGATTTCGTGTCCTCCCGCCCTTCCC 2656
Qy      619 oAsnThrAsn 622
Db      2657 CCAAGTTAGC 2666

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RESULT 16
US-10-162-012-7
; Sequence 7, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Siles-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012

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; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (1)...(1338)
; US-10-162-012-7
; US-10-162-012-7 (1-1341)
; Alignment Scores:
; Pred. No.: 2,72e-62 Length: 1341
; Score: 704.00 Matches: 157
; Percent Similarity: 57.28% Conservative: 79
; Best Local Similarity: 38.11% Mismatches: 128
; Query Match: 21.20% Indels: 48
; DB: 4 Gaps: 9

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Qy      40 GluLeuIleValIleuAsnValSerGlyArgArgPheGlnThrThrPargThrThrLeuGlu 59
Db      7 GAGCGGCTGTGTCTCAACGTGCGGGCTGTTCGAGACGCGGCGCGACGCTGGGC 66
Qy      60 ArgYrProAspThrIleuLeuGlySer---ThrGluYsgIupPhePheAsnGluAsp 78
Db      67 CGCTTCCGGAACACTCTGCTCTGAGGAGACCAAGCGCGCGCGCGCTTCTACAGACGCGC 126
Qy      79 ThrIysGluYrPhePheAspArgAspProGluValPheArgCysValIleuAsnPheYr 98
Db      127 GCGCGAGATTTCTTCTGACCGGACCGCGCCAGCTTTCAGCGCGGTGCTTACTACTAC 186

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QY ArgThr---GlyLeuHisIeTy-ProArgTyrGluCysIleSerAlaTyrAspAspGlu 117
Db 187 CAGTCCGGTGGCGGCTGGCGGCGGCGAGCGCGCTGAGCTTCTTCTGGAAGAG 246
QY 118 LeuAlaPheTyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLys 137
Db 247 GTGGCTTCTTACGGGCTGGCGGCGGCGGCGGCGA----- 282
QY 138 AspArgLysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGln 157
Db 283 ---CGCCGCGCGAG-----GACGAGGCGCTGCCCGGCGCGCGAG 321
QY 158 GluSerMetProSerLeuSerPheArgGlnThrMetTPrArgAlaPheGluAsnProHis 177
Db 322 CGCCCCCGCCCCCGGCGCTTGGCCCGCGAGCTGTGCTGCTTTCGAGTTTCCGAG 381
QY 178 ThrSerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerVal 197
Db 382 AGCTCTGAGGCGGCGGCGGCTGCTGCGGTACTTCCGCTGCTGCTGCTGCTGCTGCTC 441
QY 198 IleThrAsnValValGluThrValPro----- 206
Db 442 GTGCTTCTTCTGCTGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501
QY 207 -----CysGlyThrValPro-----GlySerLysGluLeuPro 217
Db 502 GCTGCTGAGCGCGAGCGCGCGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
QY 218 CysGlyGlu-----ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysVal 234
Db 562 GGAATCCACCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
QY 235 MetIlePheThrValGluTyrIleLeuArgLeuPheAlaAlaProSerArgTyrArgPhe 254
Db 622 TGTGTGTTCTCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
QY 255 IleArgSerValMetSerIleIleAspValAlaIleMetProTyrTyrIle----- 272
Db 682 TTCAGAACTGAGTGAACCTCATCTGATTTGTGGTATCTTCCCTACTTGTGGCACTG 741
QY 273 GlyLeuValMetThrAsnAsnGluAspValSerGlyAlaPheValThrLeu----- 289
Db 742 GGCACCGAGCTGGCGGCGAGCGAGGCTGGCGGCGAGCGAGCTGCTGCTGCTGCTGCT 801
QY 290 -----ArgValPheArgValPheArgIlePheLysPheSerArgHisSerGlnGly 306
Db 802 AGAGTATCCGATTTGATGTCGTCTTCCGATCTTCAAGCTGTCGCGCACTCAAGAGGC 861
QY 307 LeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGluLeuGlyPheLeuLeuPhe 326
Db 862 CTGCAAACTTGGCGGCGAGCGCTTCCGCGCTTCATGCTGAGCTGGGCGCTCTCATCTTT 921
QY 327 SerLeuThrMetAlaIleIlePheAlaThrValMetPheTyrAlaGluLysGlySer 346
Db 922 TTCTCTTTCATCGGTGGTGGCTCTTCTTTCAGCGCGCTTCACTTTCGGAAGTTGACCG 981
QY 347 SerAlaSerLysPheThrSerIleProAlaSerPheTyrTyrThrIleValThrMetThr 366
Db 982 GTGAGCTCCATTTCACTAGCATCCCTGAGTCTTCTGCTGGTGGCGGTGATCAGCATGCT 1041
QY 367 ThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGlyLysIlePheGlySerIle 386
Db 1042 ACAATGTGCTATGAGACATGACCCCTGCTGAGTGGAGTGAAGTGTGGGCTCTCTG 1101
QY 387 CysSerLeuSerGlyValLeuValIleAlaLeuProValProValIleValSerAsnPhe 406
Db 1102 TGTGCAATGGCGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161
QY 407 SerArgIleTyrHisGlnAsnGlnArgAlaAspLys 418
Db 1162 AGTACTTTTATCACCGGAGACAGAGGCGCAAGAG 1197

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RESULT 17
US-09-336-643A-3
Sequence 3, Application US/09336643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutler, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1927
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (105)...(1908)
OTHER INFORMATION: K+Hnov4
US-09-336-643A-3

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## Alignment Scores:

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Pred. No.: 5.1e-62 Length: 1927
Score: 704.00 Matches: 179
Percent Similarity: 49.27% Conservative: 90
Best Local Similarity: 32.78% Mismatches: 180
Query Match: 21.20% Indels: 97
DB: Gaps: 13

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US-10-062-879-4 (1-636) x US-09-336-643A-3 (1-1927)

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QY 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTPrArgThrThrLeuGlu 59
Db 126 GAGAAATCATCATCAACAGTGGGCGGCGAGCGGAGCATAGACTTACCGAGACCTCGCG 185
QY 60 ArgTyrProAspThrLeu----- 66
Db 186 ACCCTACCGGAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
QY 67 -----GlySerThrGluLysGluPhePheAsnGluAspThrLysGluTyrPhe 83
Db 246 ACCGATGGCGGCTGTGGTGAAGCGGAGCGAGCGCGCGCGGCGGCTGCGAGTTCTTC 305
QY 84 PheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArgThrGlyLysLeu 103
Db 306 TTCAGACGAGCACCGGCGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
QY 104 HisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPheTyrGlyIle 123
Db 366 CACGCGCCCGGAGACGTCGTGGGCGGCTCTTCAAGAGAGAGAGTGGCTTCTGCGGATC 425
QY 124 LeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArgLysArgGluAsn 143
Db 426 GACGAGACGAGCGTGGAGCCCTGCTGCTGATGACCTTAC-----CGGAGCACCGGAG 479
QY 144 AlaGluArgLeuMet-----AspAspAsnAsp 152
Db 480 GCCAGAGAGGCGCTGAGCATCTTGAAGACCCCGACTCATGGCGGCGAGCCCGGAGAC 539
QY 153 SerGluAsn-----AsnGlnLysSerMetProSerLeuSer----- 164
Db 540 GACGAGACCTGGCGGCGCAAGAGGCTGGGATCGAGAGACCGCGGCGGCTGCGGGGCGCC 599

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Qy 165 -----PheArgInThMetPheArgAlaPheGluAn 175
Db 600 GACGGCAATCTGCGCGTGGAGAGCGTGCAGCCCCCGCATGTGGCGCCCTTCGAAAGAC 659
Qy 176 ProHisSerThrLeuAlaLeuAlaPheTyrValThrGlyPhePheIleAlaVal 195
Db 660 CCTACTCGTCCAGAGCGCGCAGGTTATGCTTTCCTTCCTTATTCCTTACCTCGGTT 719
Qy 196 SerValIleThrAnValValGluThrValProCysGlyThrValProGlySerIysGlu 215
Db 720 TCATTTACACTTTTTCCTCGTGAACACATGAACTTCATATGTGTAATAAACAGACACA 779
Qy 216 LeuProCysGlyGluArgTyrSerVal-----Ala 225
Db 780 GAACCACTCATCAATGGACACAGGTGTGTTCTACAGTAAATGAAACGATCCTGCC 839
Qy 226 PhePheCysLeuAspThrAlaCysValMetIlePheThrValGluTyrLeuLeuArgLeu 245
Db 840 TTGACGTAATGTAAGAGAGTGTGTGTGTGTGTTTACTTTGAAATTTTAACTTCGTAAT 899
Qy 246 PheAlaAlaProSerArgTyrArgPheIleArgSerValMetSerIleIleAspValVal 265
Db 900 GTTTTTCACCCCAATAAATTGAAATTCATAAAATCTTGAAATATCATTCATTCATTGCTG 959
Qy 266 AlaIleMetProTyrTyrIle-----GlyLeuValMetThrAnAnGlu 280
Db 960 GCCATCTACCTCTTCTTACTTAAAGGTGAGCTAGTGGCGTGTCTATCCAAAGCTGTAA 1019
Qy 281 AspValSerGlyAlaPheValThrLeuArgValPheArgIlePheIysPhe 300
Db 1020 GATGTGCTGGCTTCCTCAGAGGTGTGTAAGTTGTGAGATCTCGAATTTTCAAGCTC 1079
Qy 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuIysSerCysAlaSerGlu 320
Db 1080 ACCGCGCATTTTGTAGTCTGAGGGCTCTTGACATCTCTTGAGAGTACTATTAATGAA 1139
Qy 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThrValMetPhe 340
Db 1140 TTTTGTGCTGATTAATTTTCTGGCTCTAGAGTTTGTATATTTGTACCAATGATCTAC 1199
Qy 341 TyrAlaGluIys-----GlySerSerAlaSerIysPhe 351
Db 1200 TATGCCAGAGAGAGTGGAGCTCAACCTAAGACCTTCAGCTAGTACGACACACAGCTTC 1259
Qy 352 ThrSerIleProAlaSerPheTyrTyrThrIleValThrMetThrThrLeuGlyTyrGly 371
Db 1260 AAAAACAATCCCATTTGGGTTCTGGTGGCTGTAGTACCATGACTACCTGGGTTATGGG 1319
Qy 372 AspMetValProIysThrIleAlaGlyLysIlePheGlySerIleCysSerLeuSerGly 391
Db 1320 GATATGTACCCCAACATGATGTCAGGCATCTGGTGGACCCCTGTGTCTGGCTGGA 1379
Qy 392 ValIleValIleAlaLeuProValProValIleValSerAnPheSerArgIleTyrHis 411
Db 1380 GTGCTGACATAGCAGTACGAGTCTGTCTATTCATATTTTGA--ATGTACTAC 1436
Qy 412 GluAnGlnIArgAlaAspLysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArg 431
Db 1437 TCCCTGGCAATGGCAAGACGAATACTCAAGAGAAAGAAAGAG-----CACATCCCT 1490
Qy 432 ValAlaLysThrGlySerSerAsnAlaTyrLeuHisSerIysArgAnGlyLeuLeuAn 451
Db 1491 CTTGCTCTCGAGGACGCTACCTATCTTTTGAAGACAGAAATTAATATAGGCTCGCAAT 1550
Qy 452 GluAlaLeuGluLeuThrGlyThrProGluGluHisMetGlyLysThrThrSerIle 471
Db 1551 -----AGTACACAGATGACATGTCTGGGCAAGACAAATTCACAT 1592
Qy 472 IleGluSerGlnHisIleHis-LeuLeuHisCysLeuGluLysThrThrAnHisGluPhe 491
Db 1593 CTGGA-----CATACAGATCAAGTGTATACAGTACAGCA----- 1629

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Qy 491 IleAspGluGlnMetPheGluGlnAnCysMetGluSerSerMetGlnAnTyrProse 511
Db 1630 -----GTACAGAAAGTGAAGCCGCACTATACCCCCCA 1661
Qy 511 rThrArgSerProSer 516
Db 1662 GAAAGCTCCCCATCA 1677

RESULT 18
US-08-288-405A-9
; Sequence 9, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:
; APPLICANT: Chandy, Kanthanthara G.
; APPLICANT: Kalman, Katelin
; APPLICANT: Chandy, Gilscha
; APPLICANT: Gutman, George A.
; TITLE OF INVENTION: A No. 5559009el Voltage-gated Potassium Channel
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Flehr, Hohnbach, Teest, Albritton & Herbert,
; ADDRESSER: Attn: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/WHD
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO. 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1599
; US-08-288-405A-9

Alignment Scores:
Pred. No.: 2,47e-61 Length: 1599
Score: 696.00 Matches: 177
Percent Similarity: 51.99% Conservative: 84
Best Local Similarity: 35.26% Mismatches: 166
Query Match: 20.96% Indels: 76
DB: 1 Gaps: 14

US-10-062-879-4 (1-636) x US-08-288-405A-9 (1-1599)
Qy 4 GlyValAlaAlaTyrLeuProPheAlaArg-AlaAlaAlaIleGlyTyrMetProValAl 23
Db 187 GCGGTGGGGGCGACACGTCGTTTCAACGCGTGGCGGCGGTGTGGCGCGCATAGAG---CC 243

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Db 2901 AAGCTGAGGACACAGACGAGTACTCACTTGTCTTATTTCCAGTG 2945

Search completed: April 13, 2005, 18:42:39  
Job time : 337.666 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 13, 2005, 16:04:47 ; Search time 807.439 Seconds

(without alignments)  
4778.599 Million cell updates/sec

Title: US-10-062-879-4  
Perfect score: 3320  
Sequence: 1 MAGVAAALPFAAAAGMM.....PGPNTNIPITSNVKXSVL 636

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPRO.spool\_p/US10062879/rnatc\_12042005\_113504\_17025/app\_query.fasta\_1.1614  
-DB=Published Applications NA -OPMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=Blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pcpt -THR MAX=100  
-THR MIN=0 -ALIGN=20 -MODE=LOCAL -OUTFMT=pcpt -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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Database :

Published Applications NA.\*  
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11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
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18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
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21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3300.5	99.4	2121	13	US-10-062-879-1
3	2518	75.8	2351	15	US-10-212-677-253
4	2518	75.8	2351	17	US-10-361-811-253
5	2518	75.8	2351	17	US-10-369-186-253
6	2518	75.8	2351	15	US-10-212-677-252
7	2518	75.8	2351	15	US-10-212-677-254
8	2518	75.8	5333	15	US-10-361-811-252
9	2518	75.8	5333	17	US-10-361-811-254
10	2518	75.8	5333	17	US-10-369-186-252
11	2518	75.8	5333	17	US-10-369-186-254
12	2123.5	64.0	3424	14	US-10-121-746-9
13	2090	63.0	2578	17	US-10-296-115-373
14	1658.5	50.0	5404	15	US-10-212-677-255
15	1658.5	50.0	5404	17	US-10-361-811-255
16	1658.5	50.0	5404	17	US-10-369-186-255
17	1490.5	44.9	1121	16	US-10-029-386-24777
18	887	26.7	1597	15	US-10-212-677-256
19	887	26.7	1597	17	US-10-361-811-256
20	887	26.7	1597	17	US-10-369-186-256
21	863.5	26.0	3254	15	US-10-212-677-251
22	863.5	26.0	3254	17	US-10-361-811-251
23	863.5	26.0	3254	17	US-10-369-186-251
24	856	25.8	612	9	US-09-864-761-26304
25	753	22.7	2565	17	US-10-435-935-10
26	753	22.7	3756	18	US-10-377-139-18
27	751.5	22.6	2882	18	US-10-377-139-19
28	745	22.4	2732	18	US-10-377-139-17
29	740.5	22.3	3291	17	US-10-388-934-240
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36	722.5	21.8	23055	18	US-10-322-281-94
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38	722	21.7	1371	9	US-09-974-712-3
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40	721.5	21.7	1792	9	US-09-989-920-16
41	721.5	21.7	6823	9	US-09-804-014A-7
42	721	21.7	1747	10	US-10-864-705-148
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44	717	21.6	2280	18	US-10-322-281-764
45	717	21.6	22280	18	US-10-322-281-764

## ALIGNMENTS

RESULT 1  
US-10-062-879-3  
Sequence 3, Application US/10062879  
Publication NO. US20020127649A1  
GENERAL INFORMATION:  
APPLICANT: Cockett, Mark I.  
APPLICANT: Dilks, Daniel W.  
APPLICANT: Chang Ling, Hui-Ping  
APPLICANT: Sokol, Patricia T.  
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
FILE REFERENCE: ahp-98089  
CURRENT APPLICATION NUMBER: US/10/062, 879  
PRIORITY FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US/09/176,109  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 2064

TYPE: DNA  
ORGANISM: human  
US-10-062-879-3

Alignment Scores:

Pred. No.:	0	Length:	2064
Score:	3320.00	Matches:	636
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-062-879-4 (1-636) x US-10-062-879-3 (1-2064)

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DB 73 ATGGCGGCGGAGTTGGCGCTGGCTGCTTTGGCCGGGCTGGGCGCATCGGGTGAATG 132

QY 21 ProValAlaAenCySProMetProLeuAlaProAlaAapLySaenLySaArgAlaAapGlu 40

DB 133 CCGGTGGCCCAACGTCGCCATGCCCCCTGGCCCCCGCCCAAGAACAGCGCGAGATGAG 192

QY 41 LeuIleValLeuAenValSerGlyArgArgPheGlnThrTyrArgThrThrLeuGluArg 60

DB 193 CTGATTGTCTTCAACGTGAGTGGCGGAGGTTCCAGACCTGAGAGACAGCTGAGAGCC 252

QY 61 TyrProAapThrLeuLeuGlySerThrGluLeuGluPhePheAenGluAapThrLys 80

DB 253 TACCCGAGACACCTGCTGGCGACAGCAGAGAGAGATTCTTCTTCAACGAGACACCAAG 312

QY 81 GluTyrPhePheAapArgAapProGluValPheArgCysValLeuAenPheTyrArgThr 100

DB 313 GAGTACTTCTTGCACCGGAGACCCGAGAGTGTTCGGCTGCTGCTCAACTTACCCGACG 372

QY 101 GlyLeuLeuHisTyrProArgTyrGluCysIleSerAlaTyrAapAapGluLeuAlaPhe 120

DB 373 GGGAGCTGACATACCCGCGCTAGAGTGCATCTCTGCTTACACAGCAGAGTGGCTTC 432

QY 121 TyrGlyIleLeuProGluIleIleGlyAapCysTyrGlyGluTyrLysAapArgLys 140

DB 433 TACGGCATCTCCCGGAGATCATCGGGAGATCGCTGTACAGAGATTCAGAGACCCGACG 492

QY 141 ArgGluAenAlaGluAgluAgluAgluAgluAgluAgluAgluAgluAgluAgluAglu 160

DB 493 AGGAGAGACCGCGGCGCTCATGAGACAGACACATCGAGAACCAAGAGATCTCAG 552

QY 161 ProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAenProHisTyrSerThr 180

DB 553 CCGCTCGCTCAGCTTCCGCGACACATGTGGCGGCGCTTCGAGAACCCCGACACAGACG 612

QY 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAa 200

DB 613 CTGGCCCTGGCTCTTCTACTAGTACGTGGCTTCTTCACTGCTGTGCTGCTGCTGCTGCT 672

QY 201 ValValAlaGluThrValProCysGlyThrValProGlySerIleGluLeuProCysGlyGlu 220

DB 673 GTGGTGAAGACGGGCGCTGCGGACCGCTCCGCGGCGAGAGAGAGCTGCGCGGAG 732

QY 221 ArgTyrSerValAlaPhePheCysLeuAapThrAlaCysValMetIlePheThrValGlu 240

DB 733 CGCTACTCGGTGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792

QY 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260

DB 793 TACTCTCGGGGCTTCTGCGGCTCCAGCGGCTTCAAGCGCTTCAAGCGCTTCAAGCG 852

QY 261 IleIleAapValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAaAenGlu 280

DB 853 ATCATTCAGCGTGGCGCATCATGCTTACTACATCGCTGCTGCTGCTGCTGCTGCTGCT 912

QY 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300

DB 913 GACCTGTGCGGCGCTTGTGTCAGCTCGGGCTTCTCGCGCTTTCAGAGATCTTCAAGATT 972

QY 301 SerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320

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DB 1033 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092

QY 341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTyr 360

DB 1093 TATGCCGAGAGAGGCTCTGGCGGAGAGATTCAGAGATCCCTGCTGCTGCTTGGTAC 1152

QY 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAapMetValProLysThrIleAlaGly 380

DB 1153 ACCATTGTACCATGACACACATGCGATACCGAGACATGCGCTTAAAGATTCAGAGG 1212

QY 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400

DB 1213 AAGATCTTGGCTCCATGTGCTCTTGAATGCGCTCTGATTCATTCCTGCGCATGCTCT 1272

QY 401 ValIleValSerAapPheSerArgIleTyrHisGluAenGluArgAlaAapLysArgArg 420

DB 1273 GTGATTGTTCCACTTATAGCGGATTTTACACAGATCATGAGAGCTGATTAACGACAG 1332

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DB 1333 GCACAAAGAGAGGCGCGCTTGCAGAGATCCGTGCGCAAAACAGACAGTTCAAATGCA 1392

QY 441 TyrLeuHisSerLysArgAenGlyLeuLeuAenGluAlaLeuGluLeuThrGlyThrPro 460

DB 1393 TACCTGCACAGAGCGACAGGAGCTCTTCAACAGAGCGCTGAGACTGACGAGCACCCCA 1452

QY 461 GluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHisLeuLeu 480

DB 1453 GAAAGAGAGACATGGGAGAACACCATCTATTCAGAGCCAGCATCATCCTGCTG 1512

QY 481 HisCysLeuGluLysThrThrAaHisGluPheIleAapGluGlnMetPheGluGluAa 500

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QY 501 CysMetGluSerSerMetGluAaThrProSerThrArgSerProSerLeuSerSerHis 520

DB 1573 TGCATGGAGATTCATGACAGAACCTACCATCCAGAGAGTCCCTCATCTGCGACAC 1632

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DB 1633 CCAAGCTCATCATCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1692

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DB 1693 TCTAACCTGCAGCTACTGCTGCTGCGAGCATGCAAGAGCTCACACAGATCCACATCCAG 1752

QY 561 GlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAaLeuLysAlaAapAa 580

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DB 1873 CCCCCAGCGCTAACCCCGAGAGGGGAGAAAGTGGGCGACCCCTGCGACCCCGCCCAAC 1932

QY 621 ThrAaIleProSerIleThrSerAaValValLysValSerValLeu 636

DB 1933 AGGAACATTCCTTCCATTAACAGAGATGTGTCAAGGCTCTGTGCTTG 1980

## RESULT 2

US-10-062-879-1  
Sequence 1, Application US/10062879  
Publication No. US20020127649A1

GENERAL INFORMATION:  
 APPLICANT: Cockett, Mark I.  
 APPLICANT: Dikhs, Daniel W.  
 APPLICANT: Chang Ling, Hwai-Ping  
 APPLICANT: Sokol, Patricia T.  
 TITLE OF INVENTION: Human Potassium Channel Polynucleotides and  
 FILE REFERENCE: ahp-98089  
 CURRENT APPLICATION NUMBER: US/10/062,879  
 PRIOR APPLICATION NUMBER: US/09/178,109  
 PRIOR FILING DATE: 1998-10-23  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 2121  
 TYPE: DNA  
 ORGANISM: human  
 US-10-062-879-1

Alignment Scores:  
 Pred. No.: 0 Length: 2121  
 Score: 3300.50 Matches: 636  
 Percent Similarity: 97.10% Conservative: 0  
 Best Local Similarity: 97.10% Mismatches: 0  
 Query Match: 99.41% Indels: 19  
 DB: 13 Gaps: 1

US-10-062-879-4 (1-636) x US-10-062-879-1 (1-2121)

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 21 ProValAlaAsnCyPrometProLeuAlaProAlaAspLysAsnLysArgGlnAspGlu 40  
 133 CCGGTGGCCAACTGCCCATGCCCTGGCCCGGCGGCAAGAACAGCGGAGATGAG 192  
 41 LeuIleValIleuAsnValSerGlyValArgPheGlnThrTrpAlaGlnThrLeuGluArg 60  
 193 CTGATTCTCTTCAACGTGAGTGGCGGAGGTTCCAGACCTGAGAGACACCTGGAGGCG 252  
 61 TyrProAspThrLeuLeuGlySerThrGluGluPhePheAsnGluAspThrLys 80  
 253 TACCCGACACCTCTGCTGGGACGACGAGAGAGATTCTTCTTCAACAGAGACACCAAG 312  
 81 GluTyrPhePheAspArgAspProGluValPheArgCysValIleuAsnPheTyrArgThr 100  
 313 GAGTACTTCTTCCGACCGGAGACCCGAGGTGTTCCGCTGCTCACTTCTTACCGGACG 372  
 101 GlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAlaPhe 120  
 373 GGGAGGCTGACATACCGCGCTACGAGTGCATCTCTGCTTCAACGACGAGCTGGCTTC 432  
 121 TyrGlyTyrLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArgLys 140  
 433 TACGGATCTCTCCCGAGATATCGGGAGCTGCTGCTACAGAGATTACAGACCGGACAG 492  
 141 ArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnIleSerMet 160  
 493 AGGGAGAACCGCGGCTCATGACGACCAACGACTCGAGAACCAACCAAGATCCATG 552  
 161 ProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThrSerThr 180  
 553 CCGCTGCTCAGCTTCCGACACCATGTGGGGCTTTCGAGAACCCCAACACCAACGACG 612  
 181 LeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIleThrAsn 200  
 613 CTGGCCCTGCTCTTCACTAGTACGTGCTTCTTCAACGCTGTCTCGTATACCAAC 672  
 201 ValValGluThrValProCysGlyThrValProGlySerLysGluLeuProCysGlyGlu 220  
 673 GTGGTGAGACGAGTGGCGGACCGGTCCGGGCGAGCAAGAGCTGCGTGGCGGAGG 732

221 ArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePheThrValGlu 240  
 733 CGTACTCGGTGGGCTTCTTGTGCTGGACACGGCGGTGGCTGATGATCTTACCGTGGAG 792  
 241 TyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSerValMetSer 260  
 793 TACCTCGCGGCTCTTCCGCGCTCCAGCGGCTTCAACCGGAGGCTGATGAGC 852  
 261 IleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnAsnGlu 280  
 853 ATCATTCACGTGGGTGATATCCCTACTACACGCTGCTGCTATGACCAACACAG 912  
 281 AspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheLysPhe 300  
 913 GACGTGTCGGCGGCTTGTGTCACGCTCGGCTCTCCGCGCTTCAAGATTTCAAGTTT 972  
 973 TCCGCGCACTCCAGGCGCTGGATCTGGGCTACACACTGAAGAGCTGTGCTCCGAA 1032  
 321 LeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThrValMetPhe 340  
 1033 CTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1092  
 341 TyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSerPheTrpTyr 360  
 1093 TATGCCAGAAAGGCTCTCTGCGGACGACGATTCACAAAGCATCTGCTCTTGTGATC 1152  
 361 ThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProLysThrIleAlaGly 380  
 1153 ACATTTGTACCATGACACACCTGGATACGAGACATGTGGCTTAAGACGATGGCAGGG 1212  
 381 LysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeuProValPro 400  
 1213 AAGATCTTGGCTTCATCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1272  
 401 ValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAspLysArgArg 420  
 1273 GTGATTTGTTTCACTTATGCGGATTTTCCACCAAGATCCAGAGCTGATTAACGACAG 1332  
 421 AlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySerSerAsnAla 440  
 1333 GCAAAAAGAAAGCGCGCTTGGCAGATCCGTGTGGCAAAACAGGACAGTTGCAATGCA 1392  
 441 TyrLeuHisSerLysAlaGlnGlyLeuLeuAsnGluAlaLeuGluLeuThrGlyThrPro 460  
 1393 TACCTGACAGCAAGCCCAACGGCTCTCTCAACAGAGCGCTGAGCGGACCCCA 1452  
 461 GlnGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHisLeuLeu 480  
 1453 GAAGAGAGGACATGGGCGAAGACCACTCATTCAGAGGCCAGATCATCACTGCTG 1512  
 481 HisCysLeuGluLysThrThr----- 487  
 1513 CACTGCTGGAAAAAACCATCGGTGTCTTATGATGATCCCTGTATCTGTA 1572  
 488 -----AsnHisGluPheIleAspGluGlnMetPheGluGlnAsnCys 501  
 1573 GAAACTTCACCATCAAGAAACCAAGATTATGATGAGAGAGATTGAGCAAACTGC 1632  
 502 MetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeuSerSerHisPro 521  
 1633 ATGAGAGTTTCAATGCAAGATCACTCAACAAAGATCCCTCACTGTCAGGACCA 1692  
 522 GlyLeuThrThrThrCysCysSerArgArgSerLysLysThrThrHisLeuProAsnSer 541  
 1693 GGCCTCACTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1752  
 542 AsnLeuProAlaThrArgLeuArgSerMetGlnLysSerThrIleHisIleGlnGly 561  
 1753 AACCTGCACTACTCTGCTGCGGACGATGCAAGAGCTCAGACGATTCACATCCAGGCG 1812



QY 562 SerGIuGlnProSerIleuThrThrSerArgSerSerIleuAsnIleuValAlaAspArgIY 581  
DB 1813 AGTGAAGAGCCCTCCCTCACACAGTCGCTCCAGCTTAATTGAAAGAGAGACGAG 1872  
QY 582 LeuArgProAsnCySjYrThrSerGIuGlnIleThrThraIleIleSerIleProThrPro 601  
DB 1873 CTGAGACCAAACTGCAAAACATCCAGATCACACAGCCATATCATGCAATCCCACTGCC 1932  
QY 602 ProAlaIleuThrProGIuGIYIuSerArgProProProAlaSerProGIYProAsnThr 621  
DB 1933 CCAGCGCTAACCCCAAGGGGGAGAGTCGGCCACCCCTGCCAGCCCAAGCCCAACAG 1992  
QY 622 AsnIleProSerIleThrSerAsnValIleValSerValIleu 636  
DB 1993 AACATTCCTTCATACACAGCAATGTTGCAAGGCTCTGTTCTTG 2037

## RESULT 3

US-10-212-677-253  
; Sequence 253, Application US/10212677  
; Publication No. US20030129192A1  
; GENERAL INFORMATION:  
; APPLICANT: Chenault, Ruth A.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.484C7  
; CURRENT APPLICATION NUMBER: US/10/212,677  
; CURRENT FILING DATE: 2002-08-02  
; NUMBER OF SEQ. ID NOS: 288  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ. ID NO 253  
; LENGTH: 2351  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-677-253

Alignment Scores:  
Pred. No.: 1,5e-259 Length: 2351  
Score: 2518.00 Matches: 486  
Percent Similarity: 86.58% Conservative: 69  
Best Local Similarity: 75.82% Mismatches: 70  
Query Match: 75.84% Indels: 16  
DB: Gaps: 6

US-10-062-879-4 (1-636) x US-10-212-677-253 (1-2351)

QY 1 MetAlaAlaGlyValAlaAlaATPLeuProPheAlaArgAlaAlaAlaIleGIYTPMet 20  
DB 430 ATGGCGGGGGGGGGGCGAGCGTGGCTGCTTTTGCAAGGCGACGGCTATCGGGTGAATG 489  
QY 21 ProValAlaAsnCySPrometProLeuAlaProAlaAspIleAsnIleArg---GlnAsp 39  
DB 490 CCTGTGGCTCTGGGGCTTATGCGGCTCCCCCGAGGAGAGAGAAAGAACCCCAAGAT 549  
QY 40 GluIleuIleValIleuAsnValSerGIYArgArgPheGIuThrThrArgThrIleuGlu 59  
DB 550 GCTCTATTGCTGGATGATGATGGGACCGGCTTCCAGACGTGGGAGACACCTTGAA 609  
QY 60 ArgTYrProAspThrIleuLeuGIYSerThGIuIleGIuPhePheAsnGluAspThr 79  
DB 610 CGTTAACCAACACTCTACTGCGGCACTTCTGAGAGGGGACTTTTCTTACCAACCAAGAACT 669  
QY 80 LysGIuIleuThrPhePheAspArgAspProGIuValPheArgCysValIleuAsnPheTYrArg 99  
DB 670 CAGAGATATTTCTTTGACCGTGAACCCAGACATCTTCCGCAATCCGAAATTTCTACCGC 729  
QY 100 ThrGIYIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 119  
DB 730 ACTGGGAAGCTCCACTATCTCTCGCAGAGATGATCTCTGCTTAACATGAAGAACTGGCC 789

QY 120 PheTYrGIYIleuProGIuIleIleGIYAspCysTYrGIuGIuTYrIleAspArg 139  
DB 790 TTCTTGCCCTCATCCCGAATATCATGGGACATGCTGTTTATGAGAGTACAAAGATCCG 849  
QY 140 LysArgIleuAsnAlaGIuIleuMetAspAspAsnAspSerGIuAsnAsnGIuSer 159  
DB 850 AGGCGAGAAAGCCGAGCGCTGTCAGAGACGACCGGATACCAACCGCTGGGGAGAGC 909  
QY 160 ---MetProSerIleuSerPheArgGlnThrMetThrArgAlaPheGIuAsnProIleThr 178  
DB 910 GCCTTGCCCAACATGACTGCAAGGACAGAGGTCTGGAGGGCTTCGAGAAACCCCAACAC 969  
QY 179 SerThrIleuAlaIleuValPheTYrTYrValThrGIYphePheIleAlaIleSerValIle 198  
DB 970 AGCAGATGGCCCTGGTGTCTTACTATGTCAGGGGTTTTTCAATGCGCTCTGTATC 1029  
QY 199 ThrAsnValIleuThrValProCysGIYThrValProGIYSer---LysGIuIleuPro 217  
DB 1030 GCGAATGTGTGAAGAAAGTCCGTCGGGATCAAGCCCAAGTCAATTAAAGAACTGCC 1089  
QY 218 CysGIYGIuIleuTYrSerValAlaPhePheCysIleuAspThrAlaCysValMetIlePhe 237  
DB 1090 TGTGAGAGCGGTATGCTGTGGCTTCTTGTGTGACACGGCTGCTCATGATCTTC 1149  
QY 238 ThrValGIuTYrIleuIleuArgIleuPheAlaAlaProSerArgTYrArgPheIleArgSer 257  
DB 1150 ACAGTGATGATTTGCTTCCCTGCTGCGTGCAGCGCTGATGCTTATCCCTTTGCGGAT 1209  
QY 258 ValMetSerIleIleAspValIleAlaIleMetProTYrTYrIleGIYIleuValMetThr 277  
DB 1210 GTCATGAGTATCATCGACGTGTGGCCATCTGCTTATTACATTTGGGTGATGACA 1269  
QY 278 AsnAsnGIuAspValSerGIYAlaPheValThrIleuArgValPheArgValPheArgIle 297  
DB 1270 GACATGAGGACGTGAGGGAGCTTGTGTCACTCCAGATCTCCGGCTTCAGAGATC 1329  
QY 298 PheIlePheSerArgHisSerGIuGIYIleuArgIleIleuGIYTYrThrIleuIleuSerCys 317  
DB 1330 TTTAAGTTTCCCGCATCTCAAGGCTGTGGATCTGGGATCACTGAAAGATTTGT 1389  
QY 318 AlaSerGIuIleuGIYpheIleuPheSerIleuThrMetAlaIleIleIlePheAlaThr 337  
DB 1390 GCTCAGAAATGGGCTTCTTCTTCTGCTGTCACATGGGTATCATCATCTTGCTACA 1449  
QY 338 ValMetPheTYrAlaGIuIleuGIYSerSerAlaSerIlePheThrSerIleProAlaSer 357  
DB 1450 GTTATGTTCTACGAGAGAGAGGGGCTTGGCTGCAAGTTCAACACATCCCTCGAGCC 1509  
QY 358 PheTYrTYrThrIleValIleThrMetThrThrIleuGIYTYrGIYAspMetValProIleThr 377  
DB 1510 TTCTGTATACCATGTCACATGACATGACACTTAAAGGATGATGATGATGATGATGATGAT 1569  
QY 378 IleAlaGIYIlePheGIYSerIleCysSerIleuSerGIYIleuValIleAlaIleu 397  
DB 1570 ATAGCAGGAAGATTTTGGTTTATCTGTTGCTGAGTGGGCTTGGTATGCTCTA 1629  
QY 398 ProValProValIleValSerAsnPheSerArgIleTYrHisGIuAsnGlnAlaAsp 417  
DB 1630 CCTGTTCCGGATGATGTATCAACTGATGATGATCAACCAAGATCAACGAGAGAC 1689  
QY 418 LysArgAlaGIuIleuIleuValAlaArgIleuAlaArgIleuAlaIleuValIleuIleu 437  
DB 1690 AAACGAAAGGAGCAAAAGAAAGCTGAGTGGCCAGATCCGGGAGCCAAAGGAGAAAGC 1749  
QY 438 SerAsnAlaTYrIleuHisSerIleArgAsnGIYIleuIleuAsnGIuAlaIleuGIuIleu 457  
DB 1750 GCAAAATGCTTACAGACAGAAAGAAAGTATTTCTCAATATCACTGACGCTCAAG---TCC 1806  
QY 458 GIYThrProGIuGIuIleuIleuMetGIYTYrThrThrSerIleuIleGIuSerGlnHisHis 477  
DB 1807 TCAGAGATGAGACAGGCTTTGTTAGCAAAATCCGGCTCAGCTTGAACCCACAGACAC 1866  
QY 478 HisIleuIleuHisCysIleuGIuIleuThrThrAsnHisGIuPheIleAspGIuIleuMetPhe 497

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Db 1867 CACCTGCTTACTGCTGGAAGAAAAACCAAGATCAAGAGTTTGTGGACGAAACAGTCTTT 1926
Qy 498 GUGUAGAGCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeu 517
Db 1927 GAGAGAAAGCTGACGAGAAAGTTGCACTGTTATGCTCTTCAAGTACACAGTCTTCACTG 1986
Qy 518 SerSerHisProGlyLeuThrThrThrCysCysSerArgSerLysLysThrThrHis 537
Db 1987 TCTTCAACAAGAGAGACGACAGCACTGCTGTTCAAGACGACACAAAAAAGCTTTCCG 2046
Qy 538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle 557
Db 2047 ATCCCAATGCAATGATATGACGAAAGCCATCAAGAGTATACAAAGAACTCAGACAGATT 2106
Qy 558 HisIleGlnIleSerGlnGlnIleProSerLeuThrThrSerArgSerSerLeuAsnLeuLys 577
Db 2107 CAGATCAGATGTGTGTGAGAGAACACCTCTGTCAAGCCGATCCAGTTTAAATGCCAAA 2166
Qy 578 AlaAspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrAlaIleIleSer 597
Db 2167 ATGGAAGAGTGTGTTAACTTAACTGTGAACACCTTATGTGACTACAGCAATTAATAGC 2226
Qy 598 IleProThrProProAlaLeuThrProGlnGlyGluSerArgPro-----ProProAla 615
Db 2227 ATCCCAACACCTCCAGTAAACACACCAAGAGAGAGCAGTATGCCAATCCCTGAGTAC 2286
Qy 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerVal 635
Db 2287 TCAGAGAGCA-----AATATTGTCAAGATTCTGCT 2316
Qy 636 Leu 636
Db 2317 TTG 2319

RESULT 4
US-10-361-811-253
; Sequence 253, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-253

Alignment Scores:
Pred. No.: 1.5e-259 Length: 2351
Score: 2518.00 Matches: 486
Percent Similarity: 86.58% Conservative: 69
Best Local Similarity: 75.82% Mismatches: 70
Query Match: 75.84% Indels: 16
DB: 17 Gaps: 6

US-10-062-879-4 (1-636) x US-10-361-811-253 (1-2351)
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Qy 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTyrPheThrThrLeuGlu 59
Db 550 GCTCTCATTTGCTGGAATGTGAGTGGACCCGCTTCCAGACGTGGAGGACACCTCTGAA 609
Qy 60 ArgTyrProAspThrLeuLeuGlnGlySerThrGluLysGluPhePheAsnGluAspThr 79
Db 610 GGTATCCCAAGACATCTACTGCGGAGTGTGAGAGGAACTTTTCTACACCCAGAAACT 669
Qy 80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99
Db 670 CAGCAGATTTCTTTGACCGGTGACCCAGACATCTCCGCCACATCTCGAATTTTACCGC 729
Qy 100 ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119
Db 730 ACTGGAAAGCTCCCATCTCTCCGCAAGAGATCTCTGCTTACATGAAGAACTGGCC 789
Qy 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysGlyTyrGluGluTyrLysAspArg 139
Db 790 TTTCTTGGCTCATCCCGGAAATCATGCGAGCTGTATATGAGAGTACMAAGATCGC 849
Qy 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnGlnGluSer 159
Db 850 AGCGAGAGAAAGCCGAGCGCTGACAGACGACCGGATACCAACACCGCTGGGAGAGC 909
Qy 160 ---MetProSerLeuSerPheArgGlnThrMetTyrPheAlaPheGluAsnProHisThr 178
Db 910 GCCTTGGCCACATGACTGCAAGGCAAGGAGGCTGTGAGGGGCTTGGAAACCCCAACCC 969
Qy 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
Db 970 AGCAGATGAGCCCGGTGTCTACTATGTCAAGGGGTTTTCATTCGCGCTCTGTATC 1029
Qy 199 ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
Db 1030 GCGAATGTGTGGAAGAGTGGCGGTGCGAATCAAGCCAGATCAATTAAGATCTGCC 1089
Qy 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db 1090 TGTGAGAGAGGAGTATGCTGTGTGCTTCTTGTGCTGAGACCGGCTGCTGATATCTTC 1149
Qy 238 ThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257
Db 1150 ACAATTAGATTATGCTTCCCTGGCGGACGCGCTGATGCTTATCCCTTTTGTGTCGTA 1209
Qy 258 ValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThr 277
Db 1210 GTCATGATATCATCGACGTGTGGCCATCTGCTTATTAATCATTTGGGTGATATACA 1269
Qy 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
Db 1270 GACATATGAGACGTACGCGAGGCTTTGTCACTCCGAGTCTTCCGGTCTTCAGGATC 1329
Qy 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317
Db 1330 TTTAAGTTTCCGCGCACTCTCAAGGCGCTGCGATCTCGGGATACACATGAAGAGTTGT 1389
Qy 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
Db 1390 GCCTCGAAATTTGGGCTTCTTCTTCTTCTCTCTCAACATGCTATCATCATCTTCTGCA 1449
Qy 338 ValMetPheTyrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357
Db 1450 GTTATGTTCTTACCGAGAGAGGGGCTTTCGGCTAGCAATTCACAGACATCTCCGACGCC 1509
Qy 358 PheTyrTyrThrIleValIleThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377
Db 1510 TTTCTGATATACATCGTCACATGACCACTAGGATATGTATACATGAGTGGCCAAAACC 1569
Qy 378 IleAlaGlyArgIlePheGlySerIleCysSerLeuSerLysValLeuValIleAlaLeu 397
Db 1570 ATAGCAGGAGAAATTTTGTGTCTATCTGTCTGTGAGTGGGCTTGTGATTTGCTCTA 1629
Qy 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417
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Db      1630 CCTGTTCCGATGATTTGATCTTCACTTCAGTCGATCTTACCAACGAAATCAACGAGCAAC
Qy      418  LysArgArgAlaGlnuylsyalaaArgleuAlaArgIleArgValAlaYstThrglySer
Db      1690 AAACGAAGGCGCAAAAGAAAGCTAGACTGCGCAGAGTCCGGCAGCCAAAGCGGAAAC
Qy      438  SerAsnAlaIyrieuhseryIyArgAnglyLeuLeuAngluAlaLeuGluLeuThr
Db      1750 GCAAAATGCTTACATGCAAGCAACGAAATGTTTACTCATCATCAGCTCGAG--TCC
Qy      458  G1YThrProGluGluGluIuHismetGlyIySerThrThrserLeuileGluSerGlnHis
Db      1807 TCAGAGATAGCAGGCTTTTGTGCAAAATCCGCGCTCCAGCTTTAAACCAACGACAC
Qy      478  HisLeuLeuHisIyCysleuGlnuylsyrThrThrsnHisGluPheIleAspGluMetPhe
Db      1867 CACCTGCTTACCTCGGCAAAAACCAACGATCAGAGTTGTGACGCAAGCTTT
Qy      498  GlnGlnAsnCysMetGluSerSerMetGlnAsnTYrProSerThrArgSerProSerLeu
Db      1927 GAAGAAAGCTGCAATGGAAGTTCGAACTGTTAACTGCTTCAGATCAGCTCCTTCAC
Qy      518  SerSerHisProGluLeuThrThrThrCysCysSerArgArgSerLysThrThrHis
Db      1987 TCTTCAACAACAGAGATCAGACGACCTGCTGTTCAAGACACAAACAACTTTTCC
Qy      538  LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle
Db      2047 ATCCAAATGCCAATGATATCAGAGAACCATCAAGTAGATATCAAGAACTCAGACAGATT
Qy      558  HisIleGlnIySerGluGlnProSerLeuThrThrsArgSerSerLeuAsnLeuLys
Db      2107 CAGATTCAGAGTGTGAGAGAACACCTGTCTTAACGCGCATCCAGTTTAAATGCCAA
Qy      578  AlaAspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleIleSer
Db      2167 ATGGAAGAGTGTGTTAACTTAACCTGTAACCAACTTATGTGACTACAGCAATTAATAGC
Qy      598  IleProThrProProAlaLeuThrProGluGluIyLeuSerArgPro-----ProProAla
Db      2227 ATCCAAACACCTCCAGTAACCAACACGAGAGAGATAGGCCAGAAATCCCTGAGTAC
Qy      616  SerProGlyProAsnThrAsnIleProSerIleThrsAsnValIyLysValSerVal
Db      2287 TCAGAGAGA-----AATATGTGCAGAGTTCTGCT
Qy      636  Leu 636
Db      2317 TTG 2319

RESULT 5
US-10-369-186-253
; Sequence 253, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Pfling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-253

Alignment Scores:      1.5e-259      Length:      2351
Pred. No.:

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Score:      2518.00      Matches:      486
Percent Similarity:      86.58%      Conservative:      69
Best Local Similarity:      75.82%      Mismatches:      70
Query Match:      75.84%      Indels:      16
DB:      17      Gaps:      6

US-10-062-879-4 (1-636) x US-10-369-186-253 (1-2351)
Qy      1  MetAlaAlaGlyValAlaAlaAlaTProLeuProPheAlaArgAlaAlaAlaIleGlyTyrMet
Db      430  ATGGCGCGCGGGGAGGAGCGCTGCTGCTTTTTCAGAGGGCAGCGCATCGGGTGGATG
Qy      21  ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg---GlnAsp
Db      490  CTTGTGGCTTGGGGCCCTATGCTCCGCTCCCGGAGCAAGAGAAAGAACCAAGAT
Qy      40  GlnLeuIleValIleAsnValSerGlyArgArgPheGlnThrTyrArgThrThrLeuGlu
Db      550  GCTCTCATTTGCTGAATGTAGTGGCACCCGCTTCCAGACGTGGCAGACACCTTGGAA
Qy      60  ArgTyrProAspThrThrLeuGlySerThrGluLysGluPhePheAsnGluAspThr
Db      610  CGTTACCCAGACACTTACTGGGAGTTCTGAGAGGAGCTTTTCTACCAACCCAGAAACT
Qy      80  LysGluTyrPhePheAspArgAspProGluValPheArgCysValIleAsnPheTyrArg
Db      670  CAGCAGTATTTCTTGAACGTGACCCAGACATCTTCGCAACATCTCGAAATTTCTACCGC
Qy      100  ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla
Db      730  ACTGGGAAGCTCCACTATCCCTCGCGCAGAGTGCATCTCTGTTATGATGAAGAACTGGCC
Qy      120  PheTyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArg
Db      790  TTCCTTGCCCTCATCCCGGAAATCATCGGCACCTCGTTATGAGAGTCAAGAGATCGC
Qy      140  LysArgGluAsnAlaGluTargLeuMetAspAspAsnAspSerGluAsnAsnGlnIySer
Db      850  AGGCGAGAGAAAGCGCGAGCGCTCAGACGACACCGGATTCGACCGCTGGGAGAGC
Qy      160  ---MetProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThr
Db      910  GCCTTGCCCAACATGATCGCAAGGCAAGAGGTCTGAGAGGCGCTTCCAGAAACCCCAACC
Qy      179  SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle
Db      970  AGCAGATGCGCCCTGAGTGTCTACTATGTCAGGGGTTTTTCATTCGCGTCTGTATC
Qy      199  ThrAsnValIleGluThrValProCysGlyThrValProGlySer---LysGluLeuPro
Db      1030  GCGAATGTGTGGAACAGTGCCTGCGGATCAAGCCAGGTCCATTAAGAACTGCCC
Qy      218  CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe
Db      1090  TGTGAGAGCGGTATGCTGTGGCTTCTTCTGCTTGAACAGCGCTCGCATATATCTTC
Qy      238  ThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer
Db      1150  ACAAGTTGAGTATTTGCTTCGCTGCGCTGAGCGCTGAGTGTGATTCGCGTATTC
Qy      258  ValMetSerIleIleAspValIleAlaIleMetProTyrTyrIleGlyLeuValMetThr
Db      1210  GTCATGATATATCATCAGAGTGTGGCATCTGCTTATTAACATTTGGGCTGGTATACA
Qy      278  AsnAsnGluAspValSerGlyAlaPheValThrThrLeuArgValPheArgValPheArgIle
Db      1270  GACAAATGAGAGCTGACGGAGGCTTTGTCACTCCAGAGCTTCCGGGTCTTCAGGATC
Qy      298  PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys
Db      1330  TTAAATTTTCCCGCACTCTCAAGGCTGTGGCATCTCGGGGTACACATCGAAGAGTTGT
Qy      318  AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr

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Db      1390 GCTCAGAAATGGGCTCTTCTCTTCTCGCTACCAAGCATCATCATCTCGCTACA 1449
Qy      338 ValMetPheTyrAlaGluValGlySerSerAlaSerIlePheThrSerIleProAlaSer 357
Db      1450 GTTATGTTCTACGAGAAAGGGCTTCGGCTGACCAAGTTACACAGATCCCTGACACC 1509
Qy      358 PheTyrTyrThrIleValIleThrMetThrThrLeuGlyTyrGlyAlaAspMetValProIleThr 377
Db      1510 TTCTGATACCATCGTACCATGACCACTAGGGATGTGTGACATGTGTCCAAAAACC 1569
Qy      378 IleAlaGlyIleIlePheGlySerIleCysSerLeuSerGlyValIleValIleAlaLeu 397
Db      1570 ATAGCAGGAAAGATTTTGTGTTCTATCTGTCGCTGAGTGGGGCTTGTGTCATGCTCTA 1629
Qy      398 ProValProValIleValSerAsnPheSerArgIleTyrIleGlnAsnGlnArgAlaAsp 417
Db      1630 CCTGTTCCGGTGAATGTATCCAACTTCAGTCGCTACCAACCAAGATCAACGAGCAGAC 1689
Qy      418 LysArgArgAlaGluValValAlaArgLeuAlaArgIleArgValAlaIleValThrGlySer 437
Db      1690 AAACGAAAGGCGCAAAAGAAAGCTAGACTGGCCAGGATCCGGGCGCCAAAGCGGAAAGC 1749
Qy      438 SerAsnAlaTyrLeuHisSerIleArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457
Db      1750 GCAATGCTTACATGACGAGCAACGGAATGGTTTACTCAGTAATCAGCTGACAG---TCC 1806
Qy      458 GlyThrProGluGluGluHisMetGlyIleThrThrSerLeuIleGluSerGlnHisHis 477
Db      1807 TCAGAGAGTGAAGGAGGCTTTTGTATGCAAAATCCGGCTTCAGCTTTGAAACCAGACAC 1866
Qy      478 HisLeuLeuHisCysLeuGluValThrThrAsnHisGluPheIleAsnGluGluMetPhe 497
Db      1867 CACCTGCTCACTCCTCGGAAAAAACAAGATACGAGTTGTGGAGCAAGAGCTTTT 1926
Qy      498 GluIleAsnGlyMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeu 517
Db      1927 GAAAGAAAGCTGACGAAAGTTGCAACTGTATTCGCTCTTCAAGTCAACAGTCTTCACTG 1986
Qy      518 SerSerHisProGlyLeuThrThrThrCysCysSerArgArgSerIleValThrThrHis 537
Db      1987 TCTTCAACAACAAAGATCACACAGACCTGCTTCAACAGACAAAAAAAATTTCGC 2046
Qy      538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle 557
Db      2047 ATCCCAATGCAATGTATCAAGAGCCATCAAGGTATATACAGAACTACAGACGATTT 2106
Qy      558 HisIleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuIle 577
Db      2107 CAGATTCAGATGTGTGGAGAGAAACACTCTGTCTAAGCCGATCCAGTTTAAATGCCAA 2166
Qy      578 AlaAspAspGlyLeuArgProAsnGlyAspThrSerGlnIleThrThrAlaIleIleSer 597
Db      2167 ATGGAAGAGTGTATAAAGTAACTGATGACCAACTTATGTGATACAGCATATATAGC 2226
Qy      598 IleProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAla 615
Db      2227 ATCCCAACACTCCAGTAACACACACAGAAAGAGACGATAGCCAGAAATCCCTGAGTAC 2286
Qy      616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValIleValSerVal 635
Db      2287 TCAGAGAGA-----AATATTGTGAGAGTTTCTGCT 2316
Qy      636 Leu 636
Db      2317 TTG 2319

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RESULT 6
US-10-212-677-252
; Sequence 252; Application US/10212677
; Publication No. US20030129192a1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-677-252

Alignment Scores:
Pred. No.: 5,77e-259 Length: 5333
Score: 2518.00 Matches: 486
Percent Similarity: 86.58% Conservative: 69
Best Local Similarity: 75.82% Mismatches: 70
Query Match: 75.84% Indels: 16
DB: 15 Gaps: 6

US-10-062-879-4 (1-636) x US-10-212-677-252 (1-5333)

Qy      1 MetAlaAlaGlyValAlaAlaIlePheProPheAlaArgAlaAlaIleGlyTyrMet 20
Db      966 ATGGCGGGGGGGGGGAGCGCTGGCTCCCTTTCGCAAGGGGAGGCTATCGGGGTGATG 1025
Qy      21 ProValAlaAsnGlyProMetProLeuAlaProAlaAspLysAsnLysArg---GlnAsp 39
Db      1026 CTTGTGGCTCGGGGCTTATGCTCCGCTCCCGAGGACGAGAGAGAAAGAACCAAGAT 1085
Qy      40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTyrArgThrThrLeuGlu 59
Db      1086 GCTCTATTGTGCTGAATGTAGTGGACCCGCTTCCAGAGTGGACAGACCCCTGGAA 1145
Qy      60 ArgTyrProAspThrLeuLeuGlySerThrGluIleGluPhePhePheAsnGluAspThr 79
Db      1146 CGTTACCGACGACACTCTAATGGGCGAGTCTGAGGAGACTTTTCTACACCCAGAAACT 1205
Qy      80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99
Db      1206 CAGCAGATTTCTTGTACCGGACGAGACATCTTCGACCATCTGAATTTCTACCGC 1265
Qy      100 ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119
Db      1266 ACTGGAAAGCTCCCACTATCCCGCAGAGTGCATCTGTGTTACGATGAAGAACTGGCC 1325
Qy      120 PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArg 139
Db      1326 TTTCTTGGCTCATCCCGGAAATCATGCGGACGCTGTTATGAGGAGTACAGAGATCGC 1385
Qy      140 LysArgGluAsnAlaGluValGluMetAspAspAsnAspSerGluAsnAsnGlnGluSer 159
Db      1386 AGGGAAGAAAGCGCGAGCGCTGCAAGACCGGATACCGACACCGCTGGGGAGAGC 1445
Qy      160 ---MetProSerLeuSerPheArgGlnThrMetTyrPheArgAlaPheGluAsnProHisThr 178
Db      1446 GCTTGGCCACACAGACTGCAAGGCAAGAGGTCTGAGAGGGCTTCGAGAAACCCACACCC 1505
Qy      179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
Db      1506 AGCAGATGGCCCTGAGTTCTACTATGTCACGGGGTTTTCATGTGCCGTCTGTGTCATC 1565
Qy      199 ThrAsnValAlaGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
Db      1566 GCGAATGTGGTGAACAGTGCCTGTGCGATCAAGCCAGGTCACTTAAAGAACTGGCC 1625
Qy      218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237

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Db 1626 TGTGAGAGGGATATGCTGTGCTTCTTCTGTGACACGGCCTGCGTATGATCTTC 1685  
Qy 238 ThrValGluTyrLeuLeuAaGluPheAlaAlaProSerArgTyrArgPheIleArgSer 257  
Db 1686 ACAGTTAGATGATTTGCTTCCTGCTGCGTACAGCGCTGTAGTCACTTTTGTGCTAGT 1745  
Qy 258 ValMetSerIleIleAspValIleAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
Db 1746 GTCAATGATGATCAATGAGCGTGTGCGCATCTGCTTATTAATGAGGCTGTGATGACA 1805  
Qy 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297  
Db 1806 GACATATGAGGACGTCACAGGAGCCTTTGTACACTCGCATCTTCGGGCTTCAGAGATC 1865  
Qy 298 PheIlePheSerArgIleSerGlnGlyLeuArgIleGluGlyTyrThrLeuIleSerCys 317  
Db 1866 TTTTAAAGTTTCCCGCCACTGCTCAAGGCGCTGCGTCACTGCGGATACACATGAAGAATTGG 1925  
Qy 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
Db 1926 GCCTCAAGATTTGGCTTCTTGTCTTCTGCTCAACAGGCTATCATCATCTTCGCTTAC 1985  
Qy 338 ValMetPheTyrAlaGluTyrGlySerSerAlaSerIlePheThrSerIleProAlaSer 357  
Db 1986 GTTATGTTCTACGACGAGAAAGGGGTCTTCGGCTAGCAAGTTCAACAGCATCCTCGACGC 2045  
Qy 358 PheTyrTyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIleThr 377  
Db 2046 TTTCTGATATACCATCGTACCATGACAACTAGGGATATGATGATGATGCGCAAAATCC 2105  
Qy 378 IleIleAlaGlyIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397  
Db 2106 ATACAGAGGAAGATTTTGTGTTATCTATCTGCTGAGTGGGGCTTGTGCTATGCTCTA 2165  
Qy 398 ProValProValIleValSerAsnPheSerArgIleTyrIleGluAsnGlnAlaAlaAsp 417  
Db 2166 CTTGTTCCGGTATGATATCAACTTCAGTGCATCTACACACAGATCAACAGACAGAC 2225  
Qy 418 LysArgArgAlaGluTyrIleValIleArgLeuAlaArgIleArgValAlaIleTyrGlySer 437  
Db 2226 AAACGAGAGGCGACAAAGAAAGCTAGACTGCGGCGAGATCGGCGACGAAAGCGGAGGC 2285  
Qy 438 SerIleAsnIleTyrLeuIleSerIleArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
Db 2286 GCAATATCTTACATGACAGAGCAAGCAAGGATGTTACTCATGATACAGTGCAG--TTC 2342  
Qy 458 GlyThrProGluGluGluIleMetGlyIleThrThrSerLeuIleGluSerGlnIleHis 477  
Db 2343 TCAGAGGATGACGAGGCTTTTGTAGCAATCCGCGTCCAGCTTGAAACCCAGACACAC 2402  
Qy 478 HisLeuLeuHisCysLeuGluTyrThrThrAsnHisGluPheIleAspGluGluMetPhe 497  
Db 2403 CACCTGCTTCACTCTCGAAGAAACCAAGATCAAGATTTGTGACGAAAGCTTCTT 2462  
Qy 498 GluGluAsnGlyMetGluSerSerMetGluAsnTyrProSerThrArgSerProSerLeu 517  
Db 2463 GAAGAAAGCTGACATGAGGATGCACTGTTAATGCTTCAAGTCAACATCTCTTCACTG 2522  
Qy 518 SerSerHisProGlyLeuThrThrThrCysCysSerArgArgSerIleValThrThrHis 537  
Db 2523 TCTTCAACAACAGAGACACCAAGCACTGCTTTCACAGACGACACAAAAAATCTTTCCG 2582  
Qy 538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGluGluLeuSerThrIle 557  
Db 2583 ATCCCAATGCGCATGTATACGAAAGCATCAAGGTATGATACAAAGAACTCAACAGAT 2642  
Qy 558 HisIleGlnGlySerGluGluProSerLeuThrThrSerArgSerSerLeuAsnLeuIle 577  
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Qy 578 AlaAspArgIleLeuArgProAsnCysValThrSerGlnIleThrThrAlaIleIleSer 597  
Db 2703 ATGGAAGATGTGTAACTAACTGTGAACAACCTTATGTGACTACAGAAATATATAGC 2762

Qy 538 IleProThrProProAlaLeuThrProGluGlyIleSerArgPro-----ProProAla 615  
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Qy 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValIleValSerVal 635  
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Qy 636 Leu 636  
Db 2853 TTG 2855  
RESULT 7  
US-10-212-677-254  
; Sequence 254, Application US/10212677  
; Publication No. US20030129192A1  
; GENERAL INFORMATION:  
; APPLICANT: Chenuault, Ruth A.  
; APPLICANT: Xu, Jianshun  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C7  
; CURRENT APPLICATION NUMBER: US/10/212.677  
; NUMBER OF SEQ ID NOS: 288  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 254  
; LENGTH: 5333  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-212-677-254  
Alignment Scores:  
Pred. No.: 5,77e-259 Length: 5333  
Score: 2518.00 Matches: 486  
Percent Similarity: 86.58% Conservative: 69  
Best Local Similarity: 75.82% Mismatches: 70  
Query Match: 75.84% Indels: 16  
Gaps: 6  
US-10-062-879-4 (1-636) x US-10-212-677-254 (1-5333)  
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Db 966 ATGGGCGGGGGGTGGAGCGTGGCTTGTTCAGAGGCGAGCGCTATCGGGTGAATG 1025  
Qy 21 ProValAlaAsnCysProMetProLeuAlaProAlaAspIleAsnIleValArg--GlnAsp 39  
Db 1026 CCGTGGCGCTGAGGGGCTATGCGGCTCCCGGAGCGAGAGAGAAAGAACCAAGAT 1085  
Qy 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59  
Db 1086 GCTTCATTTGCTGAAGTGAAGTGCACCGGCTTCCAGAGTGCAGACACCTTG3AA 1145  
Qy 60 ArgTyrProAspThrLeuLeuGlySerThrGluTyrGluPhePheAsnGluAspThr 79  
Db 1146 CATTACCAAGACACTTACTGGGCACTTGTGAGAGGACTTTTCTTACACCCAGAAACT 1205  
Qy 1206 CAGCAGTATTTCTTTGACCGTGAACCAAGACATCTTCGCCCAATCGTAATTTCTACGCG 1265  
Qy 100 ThrGlyIleValHisTyrProArgTyrGlyCysIleSerAlaTyrAspAspGluLeuAla 119  
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Qy 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrIleAspArg 139  
Db 1326 TTTTGGCTCATCCCGAAATCATCGGCGACTGCTGTTATGAGAGTACAGAGATCGC 1385

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QY 140 LysArgLysAsnAlaGluArgLeuMetAspAsnAspSerGluAsnAsnGlnGluSer 159
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QY 160 ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisThr 178
Db 1446 GCCTTCCCAACGATCGACGACGAGGAGGCTTGAGAGGCGCTTCGAGAAACCCCAACCC 1505
QY 179 SerThrLeuAlaLeuValPheTrpValThrGlyPhePheIleAlaValSerValIle 198
Db 1506 AGCAGCAGTGGCCGTGGTGTCTACTATGTCACGGAGTTTTCATTTGCTGCTGTCATC 1565
QY 199 ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
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QY 218 CysGlyGluArgTrpSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db 1626 TGTGAGAGCGGTATGCTGTGCTCTTCTTGTGAGACGCGCTGCGCATGATCTTC 1685
QY 238 ThrValGluTrpLeuLeuArgLeuPheAlaAlaProSerArgTrpArgPheIleArgSer 257
Db 1686 ACAGTTGAGATTGCTTGGCTGCTGCGCTGCGACGCGCTGATCGTTACCGTTTGTGCGT 1745
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Db 1746 GTCATGAGTATCATCGACGTGTGGCCATCTGCTTATTCATTTGGCTGTGATGACA 1805
QY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgIle 297
Db 1806 GACAATGAGGACGTCAGCGAGCGCTTGTTCACATCCGAGCTTCGCGGTTCAGAGATC 1865
QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTrpThrLeuLysSerCys 317
Db 1866 TTTTAAGTTTCCCGCCACTCTCAAGCGCTGCGCATCCCGGGGTACACACTGAAGAGTTGT 1925
QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
Db 1926 GCTTCAGAAATTGGGCTTGTGCTTTCCTGCTCACCAAGGATATCATCTTGCTTACA 1985
QY 338 ValMetPheTrpAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357
Db 1986 GTTATGTCTTACGAGAGAGAGGGGCTTCGCGTAGCAAGTTCAACAGATCCCTGCGAGCC 2045
QY 358 PheTrpTrpThrIleValIleThrMetThrThrLeuGlyTrpGlyAspMetValProLysThr 377
Db 2046 TTCGTGATATCATCGTCAACCATGACAACTAGGGTATGTTGATCATGTGCCCAAAACC 2105
QY 378 IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValLeuValIleAlaLeu 397
Db 2106 ATAGCAGAGGAAGATTTTGTGTTCTATCTGTTCTGATGGGGCTTGGTCAATTTGCTTA 2165
QY 398 ProValProValIleValSerAsnPheSerArgIleTrpHisGlnAsnGlnArgAlaAsp 417
Db 2166 CTTGTTCGGGTATGTTATCCAACTTCAGTGCATCTTACCCAGAAATCAACGAGCAGAC 2225
QY 418 LysArgArgAlaGlnLysLysValAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437
Db 2226 AAACGAGGGGACAAAGAAAGCTAGACTGCGCAGAACTCCGGGAGCGCAAAAGCGGAAAGC 2285
QY 438 SerAsnAlaTrpLeuHisSerLysArgAsnGlyLeuLeuAsnGlnAlaLeuGluLeuThr 457
Db 2286 GCAATATCTTACAGAGAGAAACGAGATGTTTACTCATGATACAGTCAAGCTCAG--TCC 2342
QY 458 GlyThrProGlnGlnGlnIleMetGlySerThrThrSerLeuIleGluSerGlnHis 477
Db 2343 TCAGAGAGATAGCAGGCTTTTGTTAAGCAATCCGGCTCCAGCTTTGAAACCCAGAGACAC 2402
QY 478 HisLeuLeuHisCysLeuGlnLysThrThrAsnHisGlnPheIleAspGlnGluMetPhe 497
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QY 498 GluIleAsnCysMetGluSerMetGlnAsnTrpProSerThrArgSerProSerLeu 517
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Db 2523 TCTTCACAAACAGGAGTCACAGCACTGCTGTTTCAGACAGACAAACAACTTTTCCG 2582
QY 538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle 557
Db 2583 ATCCCAATGCCATGTATGATCGAAGAGCCATCAAGTATGATACAGAACTCAGACGAT 2642
QY 558 HisIleGlnGlySerGlnGlnProSerLeuThrThrSerArgSerSerLeuAsnLys 577
Db 2643 CAGATCAGATGTGTGAGAGAAACACTGTGCTTCAAGCCGATCCAGTTTAAATGCCAA 2702
QY 578 AlaAspAspGlyLeuAspProAsnCysLysThrSerGlnIleThrAlaIleIleSer 597
Db 2703 ATGGAAGAGTGTGTTAAACTTAACTGGAACACCTTATGACTTACAGCAATATTAAGC 2762
QY 598 IleProThrProProAlaLeuThrThrProGlnGluSerArgPro-----ProProAla 615
Db 2763 ATCCCAACACTTCCAGTAAACCAACACCAAGAGAGACATAGGCCAGAAATCCCTGAGTAC 2822
QY 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerVal 635
Db 2823 TCAGAGAGA-----AATATTGTCAGAGTTTCTGCT 2852
QY 636 Leu 636
Db 2853 TTG 2855

RESULT 8
US-10-361-811-252
; Sequence 252, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-252

Alignment Scores:
Pred. No.: 5,77e-259 Length: 5333
Score: 2518.00 Matches: 486
Percent Similarity: 86.58% Conservative: 69
Best Local Similarity: 75.82% Mismatches: 70
Query Match: 75.84% Indels: 16
DB: 17 Gaps: 6

US-10-062-879-4 (1-636) x US-10-361-811-252 (1-5333)
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Db 966 ATGGCGGCGGGGAGTGGACGCGTGCCTTTTGGCAAGGAGCGGCTATCGGGTGGATG 1025
QY 21 ProValIleAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg---GlnAsp 39
Db 1026 CTTGTGCTCTCGGGGCTTATGCCGCTCCCGCCAGGACGAGAGAGAAAGAACCCAGAT 1085
QY 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59
Db 1086 GCTCTCATTTGTGTGAATGTAGTGGACCCGCTTCCAGACGTGGCAGAGACCCCTGGAA 1145

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QY 60 ArgTyrProAspThrLeuLeuGlySerThrGluLeuGluPhePheAsnGluAspThr 79  
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 QY 80 LysGluTyrPhePheAspArgProGluValPheArgCysValLeuAsnPheTyrArg 99  
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 DB 1926 GCCTCAGAAATTTGGCTTCTTCTTCTTCTGCTCAACATGCTATCATCTTCGCTTAC 1985  
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 DB 2583 ATCCCAATGCCAAATGATTCAGGAAGCCATGATAGCTGATACAAAGATCAAGCAAT 2642  
 QY 558 HisIleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLys 577  
 DB 2643 CAGATCAATGTGTGAGAGAGAAACCTCTGCTTAACAGCCGATCAGTTTAATGCCAA 2702  
 QY 578 AlaAspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrAlaIleIleSer 597  
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 QY 598 IleProThrProProAlaLeuThrProGluGlyLysSerArgPro-----ProProAla 615  
 DB 2763 ATCCCAACCTTCCAGTACACACAGAGAGACATGAGCAAGATCCCTGAGTAC 2822  
 QY 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValLysValSerVal 635  
 DB 2823 TCAGAGAGA-----AATATTGCAAGTTTCGCT 2852  
 QY 636 Leu 636  
 DB 2853 TTG 2855  
 RESULT 9  
 US-10-361-811-254  
 ; Sequence 254, Application US/10361811  
 ; Publication No. US20030206918A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Panger, Steven P.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C8  
 ; CURRENT APPLICATION NUMBER: US/10/361,811  
 ; CURRENT FILING DATE: 2003-02-05  
 ; NUMBER OF SEQ ID NOS: 293  
 ; SOFTWARE: FASTSEQ For Windows Version 4.0  
 ; SEQ ID NO 254  
 ; LENGTH: 5333  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-361-811-254  
 Alignment Scores:  
 Pred. No.: 5,77e-259 Length: 5333  
 Score: 2518.00 Matches: 486  
 Percent Similarity: 86.58% Conservative: 69  
 Best Local Similarity: 75.82% Mismatches: 70



Query Match: 75.84% Indels: 16  
DB: 17 Gaps: 6  
US-10-062-879-4 (1-636) x US-10-361-811-254 (1-5333)

QY 1 MetAlaIaGlyValAlaIaIaTrpLeuProPheAlaArgAlaAlaIleGlyTrpMet 20  
DB ATGGCGGGGGGGTGGAGCGTGGCTGCTTTGGCAAGGCGAGCGGCTATCGGGGATG 1025  
QY 21 ProValAlaAsnCySPromerProLeuAlaProAlaAspIlyAsnIlyArg---GlnAsp 39  
DB CCTGTGGCTGGGGGCTATCGCGCTCCCGGAGGCGAGAGAGAGAAAGAACCCAAAT 1085  
QY 40 GluLeuIleValIleAsnValIleSerGlyValArgPheGlnTrpArgTrpThrLeuGlu 59  
DB GCTTCATTGTGCTGAATGTAGTGGACCGCTTCCAGACGTGGACAGACACCTGGAA 1145  
QY 60 ArgTyrProAspThrIleLeuGlySerThrglulysgluphePheAsnIlyAspThr 79  
DB CGTTACCAAGACACTCTACTGGGAGTCTGAGAGGACTTTTCTACACCGAAGACT 1205  
QY 80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99  
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DB TTTCTTGGCTCATCCCGAAATCATCGGCACTGCTTATGAGGATTAAGAATGGC 1385  
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QY 140 LysArgGluAsnAlaGluArgLeuMetAspAsnAspSerGluAsnAsnGlnIleSer 159  
DB AGCGAGAGAGAGCGCGAGCGCTCGAGGACGAGCGGATACCGACACCGCTGGGAGAGC 1445  
QY 1386 AGCGAGAGAGAGCGCGAGCGCTCGAGGACGAGCGGATACCGACACCGCTGGGAGAGC 1445  
QY 160 ---MetProSerLeuSerPheArgGlnIleMetTrpArgAlaPheGluAsnProHisThr 178  
DB GCTTGGCCCAACACATGTCAGAGGAGGTCTGGAGGAGGCTTGGAGAACCCCAACCC 1505  
QY 1446 GCTTGGCCCAACACATGTCAGAGGAGGTCTGGAGGAGGCTTGGAGAACCCCAACCC 1505  
QY 179 SerThrLeuAlaLeuValPheTyrTyrValThrglyPhePheIleAlaIleValSerAlaIle 198  
DB AGCAGCAGTGGCGCTGGTGTCTTACTATGTCAAGGGGTTTTCATTTGCGCTGTCTC 1565  
QY 1506 AGCAGCAGTGGCGCTGGTGTCTTACTATGTCAAGGGGTTTTCATTTGCGCTGTCTC 1565  
QY 199 ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217  
DB GCGAATGTGTGAAACAGTGCCTGGCGGATCAAGCCAGGTCAACATTAAGAAGTGGCC 1625  
QY 1566 GCGAATGTGTGAAACAGTGCCTGGCGGATCAAGCCAGGTCAACATTAAGAAGTGGCC 1625  
QY 218 CysGlyGluArgTyrSerValAlaPhePheCysIleuAspThrAlaCysValMetIlePhe 237  
DB TGTGAGAGCGGTATGTGTGTGCTTCTTGTGTGACAGCGGCTGTGTATGATTTCTTC 1685  
QY 1626 TGTGAGAGCGGTATGTGTGTGCTTCTTGTGTGACAGCGGCTGTGTATGATTTCTTC 1685  
QY 238 ThrValGluTyrLeuLeuArgLeuPheAlaIleProSerArgTyrArgPheIleArgSer 257  
DB ACAATTGAGTATTTGCTTCCGCTGCTGACGCGCTTACCTTACCGTTTGTGTGTAGT 1745  
QY 1686 ACAATTGAGTATTTGCTTCCGCTGCTGACGCGCTTACCTTACCGTTTGTGTGTAGT 1745  
QY 258 ValMetSerIleIleAspValValAlaIleMetProTyrTyrIleGlyLeuValMetThr 277  
DB GTCATGTAGTATCATCGAGTGTGTGCTCTGCTTATTCATTTGGGCTGTGTATGACA 1805  
QY 1746 GTCATGTAGTATCATCGAGTGTGTGCTCTGCTTATTCATTTGGGCTGTGTATGACA 1805  
QY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgIle 297  
DB GACATATGAGACGTTCAGCGAGGCTTTGTGTACATCTCCAGATCTTCCGGGCTTTCA 1865  
QY 1806 GACATATGAGACGTTCAGCGAGGCTTTGTGTACATCTCCAGATCTTCCGGGCTTTCA 1865  
QY 298 PheIlyPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuIlySerCys 317  
DB TTTAAGTTTCCCGCACTCTCAAGGCTGTGCATCTCGGGGTACACACTGAAGATTGT 1925  
QY 1866 TTTAAGTTTCCCGCACTCTCAAGGCTGTGCATCTCGGGGTACACACTGAAGATTGT 1925  
QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337  
DB GCTTCAGAAATTTGGCTTCTTCTTTCGCTCAACATGAGTATCATCTGTGCTTACA 1985  
QY 1926 GCTTCAGAAATTTGGCTTCTTCTTTCGCTCAACATGAGTATCATCTGTGCTTACA 1985

QY 338 ValMetPheTyrAlaGluIlySerSerAlaSerIlyPheThrSerIleProAlaSer 357  
DB GTTATGTTTTCAGCAGAGAGAGGCTTCCGCTGAGCAAGTTTCAACAGCATCTCGAGCC 2045  
QY 358 PheTyrPyrThrIleValThrMetThrThrLeuGlyTyrGlyAspMetValProIlyThr 377  
DB TTTCTGTATTCATCTGACCATGACCATGACCACTAGAGGTATGTGACATGTGTCCAAAACC 2105  
QY 378 IleAlaGlyIleIlePheGlySerIleCysSerLeuSerGlyValIleValIleAlaLeu 397  
DB ATACAGAGAGAGATTTTGTGTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2165  
QY 2106 ATACAGAGAGAGATTTTGTGTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2165  
QY 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417  
DB CTTGTCCGGGATTTGATTCACATTCATGATGATTCATTCACCAAGATCAACGAGACAC 2225  
QY 2166 CTTGTCCGGGATTTGATTCACATTCATGATGATTCATTCACCAAGATCAACGAGACAC 2225  
QY 418 LysArgArgAlaGluIlyIlyValAlaArgLeuAlaArgIleArgValAlaIlyThrGlySer 437  
DB AAGAGAGGCGCAAAAGAAAGCTGACTGGCCAGGATCCCGGAGCGCAAAAGGAGAGC 2285  
QY 2226 AAGAGAGGCGCAAAAGAAAGCTGACTGGCCAGGATCCCGGAGCGCAAAAGGAGAGC 2285  
QY 438 SerAsnAlaTyrLeuHisSerIlySerArgAsnGlyLeuLeuAsnGluAlaLeuGluLeuThr 457  
DB GCAATGTCTTACATGACAGAGAAAGAGATGTCTTACTAGTATTCAGTGCAG---TCC 2342  
QY 2286 GCAATGTCTTACATGACAGAGAAAGAGATGTCTTACTAGTATTCAGTGCAG---TCC 2342  
QY 458 GlyThrProGluGluGluHisMetGlyIlySerThrThrSerLeuIleGluSerGlnHis 477  
DB TCAAGAGATGAGCAGGCTTTTGTATGCAATCCGCTTCAGCTTGAAGAACCAACAGCAC 2402  
QY 2343 TCAAGAGATGAGCAGGCTTTTGTATGCAATCCGCTTCAGCTTGAAGAACCAACAGCAC 2402  
QY 478 HisLeuLeuHisCysLeuGluIlyThrThrAsnHisGluPheIleAspGluGlnMetPhe 497  
DB CACCTGCTTCACTGCTCGGAGAAAGAAACAGAGATCAAGAGTTTGGAGCAAGATCTTT 2462  
QY 2403 CACCTGCTTCACTGCTCGGAGAAAGAAACAGAGATCAAGAGTTTGGAGCAAGATCTTT 2462  
QY 498 GluIlyAsnCyMetGluIlySerSerMetGlnAsnTyrProSerThrArgSerProSerLeu 517  
DB GAGAGAGGCTGATGAGAGAGTTCATCTTATGCTTCAATGCTTCAATGCTTCAATGCT 2522  
QY 2463 GAGAGAGGCTGATGAGAGAGTTCATCTTATGCTTCAATGCTTCAATGCTTCAATGCT 2522  
QY 518 SerSerHisPProGlyLeuThrThrThrCysSerSerArgSerIlyIlyThrHis 537  
DB TCTTCAACAAGAGATGACCAAGCATCTGCTTTCACAGACACCAAAAACCTTTTCCG 2582  
QY 2523 TCTTCAACAAGAGATGACCAAGCATCTGCTTTCACAGACACCAAAAACCTTTTCCG 2582  
QY 538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnIlyLeuSerThrIle 557  
DB ATCCCAATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2642  
QY 2583 ATCCCAATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2642  
QY 558 HisIleGlnIlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuIys 577  
DB CAGATCAGATGTGTGAGAGAACCTCTGTCTTACAGCCGATCAGTTTAAATGCCAAA 2702  
QY 2643 CAGATCAGATGTGTGAGAGAACCTCTGTCTTACAGCCGATCAGTTTAAATGCCAAA 2702  
QY 578 AlaAspAspGlyLeuArgProAsnCyIlySerThrSerGlnIleThrThrAlaIleIleSer 597  
DB ATGGAAGAGTGTGTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 2762  
QY 2703 ATGGAAGAGTGTGTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 2762  
QY 598 IleProThrProProAlaLeuThrProGluGlyGluSerArgPro-----ProProAla 615  
DB ATCCCAACCTTCCAGTAAACACACACAGAGAGAGACATGAGCAGATCCCTGAGTAC 2822  
QY 2763 ATCCCAACCTTCCAGTAAACACACACAGAGAGAGACATGAGCAGATCCCTGAGTAC 2822  
QY 616 SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValIlyValSerVal 635  
DB TCAGAGAGGA-----AATATGTCAAGATTTCTGCT 2852  
QY 2823 TCAGAGAGGA-----AATATGTCAAGATTTCTGCT 2852  
QY 636 Leu 636  
DB 2853 TTG 2855

RESULT 10  
US-10-369-186-252  
; Sequence 252, Application us//10369186  
; Publication No. US20030232056A1  
; GENERAL INFORMATION:  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER



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; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369.186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-252

Alignment Scores:
Pred. No.:      5,77e-259      Length:      5333
Score:          2518.00      Matches:      486
Percent Similarity: 86.58%      Conservative: 69
Best Local Similarity: 75.82%      Mismatches: 70
Query Match:    75.84%      Indels:      16
DB:             17      Gaps:      6

US-10-062-879-4 (1-636) x US-10-369-186-252 (1-5333)

QY      1  MecAlaaglyValAlaAlaATrPLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet 20
Db      966  ATGGCGGGGGGGGGGCGAGCGTGGCTGCTTTGGCAAGGGCAGCGGTATCGGGTGAGT 1025

QY      21  ProValAlaAsnCySPoMetProLeuAlaProAlaAspLysAsnLysArg--GlnAsp 39
Db      1026  CCTGTGGCTCTGGGGCTTATGCGGCTCCCGCAGGCGAGGAGGAAAGAACCCAAAGT 1085

QY      40  GluLeuIleValIleuAsnValSerGlyArgArgPheGlnThrTrpArgThrTrleuGlu 59
Db      1086  GCTCTCATTTGCTGGAATGATGATGGACACCCGCTTCAGACGTGGCAGGACACCCCTGGA 1145

QY      60  ArgTrpProAspThrTrleuLeuGlySerThrGluLysGluPhePheAsnGluAspThr 79
Db      1146  CGTTACCCAGACACTTACTGAGGAGTTCTGAGAGGACTTTTCTTACCAACCCAGAAACT 1205

QY      80  LysGluTrpPhePheAspArgAspProGluValPheArgCysValIleuAsnPheTrpArg 99
Db      1206  CAGCAGATATTTCTTTGACCGTGACCCAGACATCTTCGCGCAATCTTGAAATTTCTACCG 1265

QY      100  ThrGlyLysLeuHisTrpProArgTrpGluCysIleSerAlaTrpAspAspGluAla 119
Db      1266  ACTGGAAAGCTCCACTATCTCCGACAGAGTGACTCTGCTTACGATGAGAAAGTGGCC 1325

QY      120  PheTrpGlyLysLeuProGluIleIleGlyAspCysSerTrpGluGluTrpLysAspArg 139
Db      1326  TTCTTTGGCCTCATCCCGAAATCATCGGAGACTGGCTTATGAGGAGTACAAAGATCGC 1385

QY      140  LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSer 159
Db      1386  AGCGGAGAGAACCGCCGAGCCCTGCGAGGACGACCGCGATACCGACACCGCTGGGGAGAC 1445

QY      160  ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAsnProHisTr 178
Db      1446  GCCTTGCCCAACAGTACTGACAGGCGTGGAGGGCTTCGAGAAACCCCAACACC 1505

QY      179  SerThrLeuAlaLeuValPheTrpTrpValThrGlyPhePheIleAlaValSerValIle 198
Db      1506  AGCAGCATGGCCCTGGTGTCTTACTATGTACCGGGTTTTCATTGCGGCTCTGTCAATC 1565

QY      199  ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
Db      1566  GCCAATATGTGTGGAACAGTGCCTGCGAGTCAAGCCAGGTCACTTAAAGAACTGCCCC 1625

QY      218  CysGlyGluLysArgTrpSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db      1626  TGTGAGAGCGGATATGCTGTGGCTTCTTGTCTTGACACGGCCTGCGCATGATCTTC 1685

QY      238  ThrValGluTrpTrleuLeuArgLeuPheAlaAlaProSerArgTrpArgPheIleArgSer 257
Db      1686  ACAATTAGATTTTGTCTTCCGCTGGCTGCGACCGCTTATGTCTTACCGTTTGTGCTAGT 1745
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QY      258  ValMetSerIleIleAspValValAlaIleMetProTrpTrpIleGlyLeuValMetThr 277
Db      1746  GTCATGATATCATCAGATGATGAGTGGCCATCTGCTTATTTACATTTGGAGCTGATAGCA 1805

QY      278  AsnAsnGluAspValSerGlyValAlaPheValThrLeuArgValPheArgValPheArgIle 297
Db      1806  GACATATGAGAGCGTACGCGAGGCTTTGTCACTCCGAGTCTTCGGGGTCTTCAGATTC 1865

QY      298  PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTrpTrleuLysSerCys 317
Db      1866  TTTAAGTTTCCCGCACTTCAGAGCGCTGCGCATCTCGGGGTACACACTGAAAGATTGT 1925

QY      318  AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr 337
Db      1926  GCTCAGAAATTTGGGCTTTTCTTTCTGCTCCAGTCCAGATCATCATCTTGTGCTACA 1985

QY      338  ValMetPheTrpAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357
Db      1986  GTTATGTTCTACGAGAGAAAGGGCTTCGGCTAGCAAGTTACACAGCATCCCTGACGCC 2045

QY      358  PheTrpTrpTrpIleValIleThrMetThrThrLeuGlyTrpGlyAspMetValProLysThr 377
Db      2046  TTCTGATATACATCTGCATGACATGACAACTAGGGTATGGTACATGTGTCACAAAAACC 2105

QY      378  IleAlaGlyLysIlePheGlySerIleCysSerLeuSerGlyValIleuValIleAlaLeu 397
Db      2106  ATAGCAGGAAAGATTTTGTGTTCTATCTGTTCGTGAGTGGGGGCTTGTGATATGCTCTA 2165

QY      398  ProValProValIleValSerAsnPheSerArgIleTrpHisGlnAsnGlnArgAlaAsp 417
Db      2166  CCTGTTCGGGATTTGTATTCACATTCAGTGCATCTTACCCAGATTCACCAAGATCCAGCGAC 2225

QY      418  LysArgArgAlaGlnLysLysAlaArgLeuAlaArgIleArgValAlaLysThrGlySer 437
Db      2226  AAACCAAGGGCAGAAAGAAAGCTAGACTGGCCAGAGATCCCGGAGCGCAAAAGCGGAAAGC 2285

QY      438  SerAsnAlaTrpLeuHisSerLysArgAsnLysLeuLeuAsnGluAlaIleuGluLeuThr 457
Db      2286  GCAATATGCTTACATCAGAGCAAAACGGAATGTTTACTCATGATATCAGCTGCAG--TCC 2342

QY      458  GlyThrProGluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHis 477
Db      2343  TCAAGAGATGAGAGGCTTTTGTATGCAAACTCCGGCTCCAGCTTGAACCCAGACACAC 2402

QY      478  HisLeuLeuHisCysLeuGluLysThrThrAsnHisGluPheIleAspGluGlnMetPhe 497
Db      2403  CACTGCTTCACTGGCTGAGAAACCAAGATCAGAGTGTGGAGCAAGCAAGTCTTT 2462

QY      498  GlnGlnAsnCysMetGluSerSerMetGlnAsnTrpProSerThrArgSerProSerLeu 517
Db      2463  GAAGAAAGCTGATGGAAGTTGCACTGTTATGTCTTCAAGTCAACAGTCTTCACTG 2522

QY      518  SerSerHisPProGlyLeuThrThrCysCysSerArgArgSerLysLysThrThrHis 537
Db      2523  TCTTCAACAACAAGAGTACCAAGACCTGCTGTTCACAGACACACAAAAAATCTTTCGC 2582

QY      538  LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnGluLeuSerThrIle 557
Db      2583  ATCCCAAAATGCAATATGATCAAGAAAGCATCAGATGATATACAAAGATCAGACAGATT 2642

QY      558  HisIleGlnGlySerGluGlnProSerLeuThrThrSerArgSerSerLeuAsnLeuLys 577
Db      2643  CAGATCAATATGTTGAGAGAACACCTCTGTCTGACAGCCCATCAGTTTAAAGCCAAA 2702

QY      578  AlaAspAspGlyLeuArgProAsnCysLysThrSerGlnIleThrThrAlaIleIleSer 597
Db      2703  ATGGAAGGTGTGTTAACTTAACTGTGACAAACCTTATGTGATCTACAGCAATATTAAGC 2762

QY      598  IleProThrProProAlaLeuThrProGluLysGluSerArgPro-----ProProAla 615
Db      2763  ATCCCAACACCTCCAGTAAACCAACACAGAGAGACATAGCCAGAAATCCCTCGAGTAC 2822

QY      616  SerProGlyProAsnThrAsnIleProSerIleThrSerAsnValValLysValSerVal 635
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Db 2823 TCAGAGAGA-----AAATATGTCAGAGTTTGCT 2852
Qy 636 Leu 636
Db 2853 TTG 2855

RESULT 11
US-10-369-186-254
; Sequence 254, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-254

Alignment Scores:
Pred. No.: 5.77e-259 Length: 5333
Score: 2518.00 Matches: 486
Percent Similarity: 86.58% Conservative: 69
Best Local Similarity: 75.82% Mismatches: 70
Query Match: 17 Gaps: 6
DB: 17

US-10-062-879-4 (1-636) x US-10-369-186-254 (1-5333)
Qy 1 MecAlaIaGlyValAlaAlaTrpLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet 20
Db 966 ATGGCGCGGGGAGTGGGAGCGCTGGCTTTGGCAAGCGGCGCTATGGGTGATG 1025
Qy 21 ProValAlaAsnCysProMetProLeuAlaProAlaAsnIleValArg---GlnAsp 39
Db 1026 CCGTGGCGCTCGGGCGCTATGCCGGCTCCCGCGAGCGAGAGAGAAAGACCAAGAT 1085
Qy 40 GluLeuIleValIleAsnValSerGlyArgArgPheGlnThrTrpArgThrThleuGlu 59
Db 1086 GCTCTCATTTGCTGAATGTGATGGGCACCGCTTCCAGACGTGGCAGACACCTGGAA 1145
Qy 60 ArgTrpProAspThrLeuLeuGlySerThrGluIleGluPhePhePheAsnGluAspThr 79
Db 1146 CGTTACCAAGACACTTACTGAGGAGTCTGAGAGGAGCTTTTCTTACACCGAAGAACT 1205
Qy 80 LysGluIlePhePheAspArgAspProGluValPheArgCysValIleAsnPheTyrArg 99
Db 1206 CAGAGATATTTCTTGAACCGGAGCCAGACATCTTCCGCCACATCTGAATTTCTACCGC 1265
Qy 100 ThrGlyIleLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119
Db 1266 ACTGGGAAGCTCCACTATCTCCGCCACAGTGCATCTCTCTGATGAAGAACTGGCC 1325
Qy 120 PheTrpGlyIleLeuProGluIleIleGlyAspCysTyrGluIleTyrIleAspArg 139
Db 1326 TTTCTTGGCTCCATCCCGAAGATCATCGGCGACTGCTGTATAGAGAGTACAAAGATCGC 1385
Qy 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSer 159
Db 1386 AGGGAAGAGAAACCGCGAGCGCTGAGAGACGACCGGATACCAACCGCTGGGGAAGGC 1445
Qy 160 ---MetProSerLeuSerPheArgGlnThrMetTrpAlaIlePheGluAsnProHisThr 178
Db 1446 GCCTTGGCCACATGACTGCAGAGCAAGGAGGTCTGAGAGGCTTTCGAGAAACCCCAACCC 1505
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Qy 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
Db 1506 AGCAGCATGGCCCTGGTGTCTACTATGTCAGCGGGGTATTTTCATGGCGTCTGTCTATC 1565
Qy 199 ThrAsnValValGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
Db 1566 GCGAATGTGTGGAACAGTGCCTGGCGAATCAAGCCAGGTCACTTAAGAAAGCTGGCC 1625
Qy 218 CysGlyIleArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db 1626 TGTGAGAGCGGTATGCTGTGGCTTCTTCTGTCTTGGACAGCGCTGGTCAATATCTTC 1685
Qy 238 ThrValGluIleLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257
Db 1686 ACAGTTGAGTATTTGCTTGGCTGGCTGAGCGCTGATGCTTACCGTTTGTGGTGAAT 1745
Qy 258 ValMetSerIleLeuAspValAlaIleMetProTyrTyrIleGlyLeuValMetThr 277
Db 1746 GTCATGAGTATCATGACGATGTGGCCATCTGCTTATTAATTTGAGGCTGGTATGACA 1805
Qy 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
Db 1806 GACATGAGAGCGTACAGCGAGCTTTGTCACTCCAGTCTTCCGGTCTTACAGATC 1865
Qy 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLeuLysSerCys 317
Db 1866 TTTAAGTTTCCCGCACTCTCAAGGCTGGCATCTCGGGGTACACACTGAAGAGTTGT 1925
Qy 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
Db 1926 GCCTCAAGATTTGGCTTCTGCTTTTCGCTCAACATGGTATCATCATCTTTGGCAACA 1985
Qy 338 ValMetPheTyrAlaGluIleValSerSerAlaSerLysPheThrSerIleProAlaSer 357
Db 1986 GTTATGTTCTTACGAGAGAGAGGCTTTCGGCTGCAAGTTCACACAGCATCTCTGACGC 2045
Qy 358 PheTrpTyrThrIleValIleThrMetThrThrLeuGlyTyrGlyAspMetValProLysThr 377
Db 2046 TTTCTGTTATACATCGTACCATGACATGACAACTAGGATGTGATGATGTCGCAAAACC 2105
Qy 378 IleAlaGlyIleValIlePheGlySerIleCysSerLeuSerGlyValIleValIleAlaLeu 397
Db 2106 ATAGCAGGAGAAATTTTGGTTATCTGTTCCGTGAGTGGGCTTGGTATGCTCTA 2165
Qy 398 ProValProValIleValSerAsnPheSerArgIleTyrHisGlnAsnGlnArgAlaAsp 417
Db 2166 CCGTGTCCGGATGTGATTCCACTTCACTGATGCTTACCAACGAAATCAACGAGCAGAC 2225
Qy 418 LysArgArgAlaGluIleValIleValIleValIleValIleValIleValIleValIleVal 437
Db 2226 AAACGAAGGCGCAAAAGAAAGCTAGCTAGCTGGCCAGATCCGGGAGCCAAAGCGGAAGC 2285
Qy 438 SerAsnAlaTyrIleuHisSerIleValArgAsnGlyLeuLeuAsnGluAlaLeuThr 457
Db 2286 GCAATGCTTACATGAGAGAGAAACGAAATGGTTTACTAGTATACAGTCCAG---TCC 2342
Qy 458 GlyThrProGluGluGluIleMetGlyIleThrThrSerLeuIleGluSerGlnHisHis 477
Db 2343 TCAGAGANTGAGCGGGCTTTTGTAGCAAAATCCGGCTTCAAGCTTTGAAACCCAGACAC 2402
Qy 478 HisLeuLeuHisCysLeuGluIleThrThrAsnHisGluPheIleAspGluGlnMetPhe 497
Db 2403 CACTGCTTCACTGCTGGAAAAAACAAGATACAGATTTTGAGAGCAAGATCTTT 2462
Qy 498 GluIleAsnCysMetGluSerSerMetGlnAsnTyrProSerThrArgSerProSerLeu 517
Db 2463 GAAGAAAGCTGATGAGAAAGTTGCAACTGTAAATGCTCTTCAAGTCAAGCTCTTCACTG 2522
Qy 518 SerSerHisProGlyLeuThrThrThrCysCysSerSerArgSerIleValIleThrHis 537
Db 2523 TCTTCAACAACAGGAGTACACACTGCTGTTCAGAGACACAAAAAACCTTTTCC 2582
Qy 538 LeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnIleLeuSerThrIle 557
```



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QY 395 11eAlaLeuProValProVal11eValSerAnPheSerArg1LeuYH1eG1nAsnG1n 414
DB 1454 ATTGCCCTGCTGTCAGCATATGTGTCCAACTTTAGCCGCACTTACCACCAAGACAG 1513
QY 415 Arg1AaPlyArgArg1AeG1nLyVal1AaArg1eValAaArg1eValAaArg1eVal 434
DB 1514 CGGGCTGACAAAGCCCGAGCAGACAGAAAGGTGGCTGGCAAGATCCGATGGCAAG 1573
QY 435 Thr1LySerSerAn1A1TyLeuH1eSer1yAaArgAnG1yLeuAAsnG1uAlaLeu 454
DB 1574 AGTGGTACACCAATGCTTCTGCAAGCAAGAAATGG3-----GGCCTT 1621
QY 455 GluLeuThrG1yThrProGluGluG1nH1eMet---G1yLeuThrThrSer1eU1eG1u 473
DB 1622 GAGACACAGCCGATGCGAGAAAGAGCTTTGTGTGACAGAACCTTGTGCTTGA 1681
QY 474 SerG1nH1eVal1eVal1eVal1eVal1eVal1eVal1eVal1eVal1eVal1eVal 493
DB 1682 CAGCAACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741
QY 494 GluGlnMetPheGluGlnAsnCyMetGluSerMetGlnAsnTyProSerThrArg 513
DB 1742 GAGTCACTTCACTGAA---GCCCTGGAGCCCTGCTGCGCGGTGGCCGACACCGCT 1798
QY 514 SerProSerLeuSerAnH1ePro-----G1yLeuThrThrThrCysCysSer 529
DB 1799 AGCACTTGTGTCTTCCAGCAGTGGAGACCCGAGACCTGTGTCTTGTGCTGCT 1858
QY 530 ArgArgSer1yS---LysThrThrH1eValProAnSerAnLeuProAlaThrArgLeu 548
DB 1859 CGCAGGCGCAGAGCCCGCCGATCCGCTTCCAACTCCACTGCTGCTGCTGCTGCT 1915
QY 549 ArgSerMetGlnGluSerThr1LeH1eG1nG1ySerG1uGlnProSerLeuThr 568
DB 1916 GAGCGCATGAGAGCTGACATG-----CTGGCAGGCGTGGCAGAGGACATGCCCT 1969
QY 569 ThrSerArgSerSerLeuAnLeuValAaAspArg1yLeuAArgProAnCysValThr 588
DB 1970 CAGAGCGCTCAGCTCAATAGCCAGGCCCATGACGCTTACCTGACCTGACAGC 2029
QY 589 SerGln1eThrAla1eAla1eSer1eProThrProProAlaLeuThrProGluGly 608
DB 2030 CGGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2086
QY 609 GluSerArgProProAlaSerProGly----- 618
DB 2087 GAGAGCCAA-----CCTTCTCCCTGGCGGCGGTGCGAGGCGGAGCACCTTCAG 2140
QY 619 ---ProAnThrAn1eProSer1eThrSerAnVal1yValSerValLeu 636
DB 2141 AACTCCAGCTGGTACCTTGGCTTCTCCCGAGACTGTCAAGATCATCCCTG 2197

RESULT 13
US-10-296-115-373
; Sequence 373, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 373
; LENGTH: 2578
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-373

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Alignment Scores:
Pred. No.: 1,86e-213 Length: 2578
Score: 2090.00 Matches: 426
Percent Similarity: 77.16% Conservative: 84
Best Local Similarity: 64.45% Mismatch: 115
Query Match: 62.95% Indels: 37
DB: 17 Gaps: 13

US-10-062-879-4 (1-636) x US-10-296-115-373 (1-2578)
QY 1 Met1Aa1eG1yVal1Aa1A1eP1eUProPhe1Aa1Aa1Aa1eG1yT1P1eMet 20
DB 1 ATGGCGGACAGGCTGGCCAGCAGCTGCTGCTTGTCTGCGGACAGCAGAGTGGCTGCTG 60
QY 21 ProVal1AaAnCySPrometProLeu1A1Pro1AaPlyAaAn1yAaArg1AaAspG1u 40
DB 61 CCCCTGGCCAGCAACCTGCTCCCGCCAGCCGGGGGTAAAGGCAATCTCGAGAGATGAG 120
QY 41 Leu1eVal1eAnVal1eSerG1yArgArgPheG1nH1eThr1P1eArg1yThr1eU1eValArg 60
DB 121 GTTCTGTGTGTAACGTGAGCGAGCGCGCTTGAAGCTTGAAGATATGCTGAGCCGC 180
QY 61 TyrProAspThrLeuLeuGlySerThrGluGluGluPhePheAnGluAspThr1yS 80
DB 181 TACCAGACACCTTGTGGGAGCTCGAGAGAGAAATTTCTTCAAGATGCTGACTCAGGC 240
QY 81 GluTyRhePheAspArgAspProGluValPheArgCysVal1eAnPheTyRArgThr 100
DB 241 GAGTACTTCTTCATCCGACCCGACATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 300
QY 101 Gly1ySer1eH1eVal1eProArg1yGluCys1eSer1eVal1eAspAspGluLeu1A1Phe 120
DB 301 GGGGCGCTGATTCCTCCAGCGCAGAGATGATCCAGGCTTTCGAGAGAGCTGCTTTC 360
QY 121 TyrG1y1eLeuProGlu1e1eG1yAspCys1yGluGluTyRAspArg1yS 140
DB 361 TAGCGCTGCTGCTCCGAGCTAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 141 Arg1eAn1AaG1uA1eGluMetAspAspAnAspSerG1uAnAnGlnGluSerMet 160
DB 421 AAGGAGATGCGCGCCCTGGCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
QY 161 ProSerLeu-----SerPheArgGlnH1eMet1P1eArg1A1ePheG1uAsnPro 176
DB 478 CCAGCTTCCAGCAGGAGCTCTCTGCGGAGCGCTGCGGCTTGAAGATCCA 537
QY 177 HisThrSerThrLeu1A1eVal1PheTyR1yVal1ThrG1yPhePhe1eAla1eValSer 196
DB 538 CAGACGAGCACCGGAGCGCTGTTTCTAATGTGACCGGCTTCTCATGCGCGTGC 597
QY 197 Val1eThrAnVal1A1GluThrVal1ProCys-----G1yH1eValProGlySer1yS 214
DB 598 GTCATCCCAATGTGTGTGAGACCATCCATGCGCGGCTTGCAGCAGCAGCTCTCAAG 657
QY 215 GluLeuProCysG1yGluArgTySerVal1A1ePheCys1eAnAspThr1A1eCysVal 234
DB 658 GAGCAGCGCTGTGGAGAGCTTCCACAGGCTTTTGTGATGACAGAGCTGTGTA 717
QY 235 Met1ePheThrVal1GluTyRLeuLeuArgPheAn1A1eProSerArgTyRArgPhe 254
DB 718 CTCATATTCACAGGTGAATCTCTGCGGTGTTCCGCGCCAGCGGTGCGGCTTC 777
QY 255 11eArgSerVal1eMetSer1e1e1eAspVal1A1e1eMetProTyR1y1eG1yLeu 274
DB 778 CTGCGAGGTGTCAAGACCTCATGAGTGTGTGCTTCTGCTTCTCATGAGGCTT 837
QY 275 ValMetThrAnAnGluAspVal1eSerG1yAlaPheVal1Thr1eAnGval1PheArgVal 294
DB 838 TTGATGCCCAAGACAGATGTCTTGGCGCTTGTACCTGCTGCTGCTGCTGCTGCTGCTG 897
QY 295 PheArg1ePhe1ySPheSerArg1eSerGlnG1yLeuArg1eGluG1yTyRThr1eU 314

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Db 898 TTTCGACATCTTCAAGTTCTCCAGGCACTCAAGGGCTTGAGATTCTGGGCTACAGACTC 957  
 Qy 315 LysSerCysAlaSerGluLeuGlyPheLeuLeuPheSerLeuThreMetAlaIleIle 334  
 Db 958 AAGGCTGTGCTCTGAGTGGGCTTTCTCTCTTTCTCTTACCAATGAGCCATCATC 1017  
 Qy 335 PheAlaThrValMetPheTyrAlaGluLeuGlySerSerLeuAspSerPheThrSerIle 354  
 Db 1018 TTTCGACATCTGCAATGTTTAAAGCTGAGAGAGGCAACAACAAACCACTTACCAAGCATC 1077  
 Qy 355 ProAlaSerPheThrTyrThrIleValThreMetThrLeuGlyTyrGlyAspMetVal 374  
 Db 1078 CTGCGGCTCTTCTGATACCATTTGATCAGATGACCAAGCTTGCGTACGAGACATGGG 1137  
 Qy 375 ProLeuThrIleAlaGlyLeuIlePheGlySerIleCysSerLeuSerGlyValLeuVal 394  
 Db 1138 CCCAGACACCATGCTGGCAGAGATTTTGGGCTCATGCTGACATGCTGAGTGGCGCTTGATC 1197  
 Qy 395 IleAlaLeuProValProValIleValSerAspPheSerArgIleTyrThrIleGlnAsnGln 414  
 Db 1198 ATTGCGCTGCTGCGCAGATCATTTGTTCCAACTTAAAGCCGATCTACCAACAGAACCAAG 1257  
 Qy 415 ArgAlaSerLysArgAlaGluAlaGluLeuValArgLeuAlaArgIleArgValAlaVal 434  
 Db 1258 CGGCTGACAAAGCCCGAGACAGACAGACAGAGTGGCTTGCCAGATCCGATTTGGGCAAG 1317  
 Qy 435 ThrGlySerSerAsnAlaTyrLeuHisSerLysArgAsnGlyLeuLeuAsnGlyAlaLeu 454  
 Db 1318 AGTGTGACCAACCATGCTCTTCTGCACTGACATACAGACAGATGGG-----GGCCTT 1365  
 Qy 455 GluLeuThrGlyThrProGlnGluGlnIleMet---GlyLeuThrThrSerLeuIleGln 473  
 Db 1366 GAGGACACGGGCGAGAGAGAGAGAGAGAGCTGTTGTTGTCAGAAACCGTTTGCTTTGAA 1425  
 Qy 474 SerGlnIleValIleValLeuLeuHisCysValLeuGlyLeuThrThrAsnIleGluPheIleAsp 493  
 Db 1426 CAGCAATCATCAACCTTGTGCACTGTCTAGAGAAAGCAACGTGACATGATTCACAGAT 1485  
 Qy 494 GluIleMetPheGlnIleAsnValAsnValCysMetCysSerSerMetGlnAsnTyrProSerThrArg 513  
 Db 1486 GAGCTCACTTCAATGAA---GCCCTGGAGACCGTCTCGCGGAGTGGCCGACCAACCGCT 1542  
 Qy 514 SerProSerLeuSerSerHisPro-----GlyLeuThrThrThrCysCysSer 529  
 Db 1543 AGCACTCTGTGTCTTCCAGCCAGTGGAGCCGGAAGCTGTGCTGTCTTCTGCTCCCT 1602  
 Qy 530 ArgArgSerLys---LysThrThrIleLeuProAsnSerAsnLeuProAlaThrArgLeu 548  
 Db 1603 CGCAGGGCCAAAGCCCGCCGATCCGCTTGCACATCCA--CTGCTCAGTCAAGCCGTG 1660  
 Qy 549 ArgSerMetGlnIleLeuSerThrIleIleIleGlnGly---SerGlnGlnProSerLeu 567  
 Db 1661 GCAGGAGTGCAGAGTGCAGATG-----CTGGCAGAGCTTGGCGAGGAGCATGCCCC 1714  
 Qy 568 ThrThrSerArgSerSerLeuAsnLeuValAlaAspArgIleLeuArgProAsnCysLeu 587  
 Db 1715 TTCAGACCCGCTCCAGCTTCAATGCAAGCCCAATACAGCTTGAACCTGAACCTGAGAC 1774  
 Qy 588 Thr-SerGlnIleThrThrAlaIleIleSerIleProThrProProAlaLeuThrProG 607  
 Db 1775 AGCGGGGAGACTTCTGCTGCTGATTCACAGATCCCTACCCCTCTGCGCAACCCCAAG 1834  
 Qy 607 uGlyGluSerArgProProProAlaSerProGly----- 618  
 Db 1835 T---GAGAGCCAA-----CCTTCTCTCCCTGGGCGGAGTGGAGGGCCGCGAGACCTT 1885  
 Qy 619 -----ProAsnThrAsnIleProSerIleThrSerAsnValValIleValSerValIle 636  
 Db 1886 CAGGAACTCAGCCTGGGATACCTTGTCTTCCCGAGACTGTCAAGATCTCATCCCT 1945  
 Qy 636 u 636  
 Db 1946 G 1946

RESULT 14  
 US-10-212-677-255  
 ; Sequence 255, Application US/10212677  
 ; Publication No. US20030129192A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chenault, Ruth A.  
 ; APPLICANT: Xu, Jiongchun  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Harlocker, Susan J.  
 ; APPLICANT: McNeill, Patricia D.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.484C7  
 ; CURRENT APPLICATION NUMBER: US/10/212.677  
 ; CURRENT FILING DATE: 2002-08-02  
 ; NUMBER OF SEQ ID NOS: 288  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 255  
 ; LENGTH: 5404  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-212-677-255  
 Alignment Scores:  
 Pred. No.: 1.59e-166 Length: 5404  
 Score: 1658.50 Matches: 320  
 Percent Similarity: 87.71% Conservative: 37  
 Best Local Similarity: 78.62% Mismatches: 33  
 Query Match: 49.95% Indels: 17  
 Gaps: 5  
 US-10-062-879-4 (1-636) x US-10-212-677-255 (1-5404)  
 Qy 1 MetAlaAlaGlyValAlaAlaAlaTrpLeuProPheAlaArgAlaAlaAlaIleGlyTyrMet 20  
 Db 1369 ATGGGCGGGGGGGTGGCAGCGCTGCTGCTTTTGCAGGGGAGGCGGTATCGGGTGATG 1428  
 Qy 21 ProValAlaAsnValCysProMetProLeuAlaProAlaAspLysAsnValArg---GlnAsp 39  
 Db 1429 CCTGTGGCTGCGGGGCGCTATGCGGGCTCCCGAGGAGGAGAGAGAAAGGACCAAGAT 1488  
 Qy 40 GluLeuIleValIleAsnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59  
 Db 1489 GCTTCATTTGCTGAATGATGAGTGCACCCGCTTCCAGACGTGCGACAGACCTTGAA 1548  
 Qy 60 ArgTyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThr 79  
 Db 1549 CATTACCAAGACACTCTACTGCGGAGTTCAGAGGAGCACTTTTCTACACCCAGAAACT 1608  
 Qy 80 LysGluTyrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99  
 Db 1609 CAGCAGATTTCTTTGACCGTGAACCCAGACATCTTCCGCGCACCTGAATTTCTACCGC 1668  
 Qy 100 ThrGlyLysIleHisTyrProArgTyrGluCysIleSerIleTyrAspArgIleLeuAla 119  
 Db 1669 ACTGGAGATCTCACTACTCTGCGCAGAGGATCTCTGTGTTACATGAAGAACTGACC 1728  
 Qy 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrTyrLysAspArg 139  
 Db 1729 TTCTTGGCTCTATCCCGGAATCATCGGCGCATGCTGTTATGAGAGTACAAAGATCCG 1788  
 Qy 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnIleSer 159  
 Db 1789 AGGCGAGAGAGAGCGGAGCGCTGACAGGACGACCGGATACCGACACCGCTGGGAGAGC 1848  
 Qy 160 ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGlnIleAsnProHisThr 178  
 Db 1849 GCGTTGCCACACATGACGCAAGGAGAGGCTCTGGAGGGCTTTCGAAACCCCAACACC 1908  
 Qy 179 SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198  
 Db 1909 AGCAGATGGCCCTGGTGTCTACTATGTCAAGGGGTTTTTTCATTGCGCTCTGTATATC 1968

Qy		199	ThrmEnVal1aGluThrValProCysGlyThrValProGlySer---	LysGluLeuPro	217
Db		1969	GCGAATGTGGTGGAAACAGTCGCCGTCCGGAATCAAGCCAGCTCACATTAAAGAATCGCCC		2028
Qy		218	CysGlyJuArGTYrSerValAlaBpheCysLeuAspThrAlaCysValMetIlePhe		237
Db		2029	TGTGGAGACGGTATGCTGTGGCCCTTCTTGCTTGAGACAAGGCCTGCATCATGATCTTC		2088
Qy		238	ThrValGluYrIleLeuArgLeuPheAlaIleProSerArgYrArgPheLeuArgSer		257
Db		2089	ACAGTTGAGYrTTTGCTTCGGCTCGCTCCAGAGCCCTAATGCTTACCGTTTTGTGGTAGT		2148
Qy		258	ValMetSerIleIleAspValValAlaIleMetProTYrYrIleGlyLeuValMetThr		277
Db		2149	GTCATGAGTATCATCGACGTGTGGCCATCTCGCTTATTCATTGGGCTGTGTATGACA		2208
Qy		278	AsnAngIuaApvalSerGlyAlaBpheValThrLeuArgValPheArgValPheArgIle		297
Db		2209	GACATATGAGACGTCACGGCAGCCCTTGTCAACATCCAGACTTCGCCGATCTTCAGAGATC		2266
Qy		298	PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyYrThrLeuLysSerCys		317
Db		2269	TTTAAGTTTCCCCGCACTCTCAAGGCTCGGCACTCGGGGTACACATAAGAGTGT		2328
Qy		318	AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIlePheAlaThr		337
Db		2329	GCCTCAGAAATGGGGCTTCTTGCTTTCTCGCTACACATGGCTATCATCTGTGCTACA		2388
Qy		338	ValMetPheTYrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer		357
Db		2389	GTTATGTCTTACGACGAGAAAGGGCTTCGGCTAGCAAGTTCAACAGCATCCCTGCACGC		2448
Qy		358	PheTrPYrThrIleValIleThrMetThr-----		367
Db		2449	TTCTGATATCATCTGTCAACATGACAACACTAGGGTAGTGCCATATGGGAATGGGA		2508
Qy		368	----LeuGlyTYrGlyAspMetVal-----ProLysThrIleAlaGlyLysIlePhe		383
Db		2509	TGGAGTGTGGGTATGGGTGAGAGCGCATGTGTGACCATCGAGGTATCATGTAACTCCGGG		2568
Qy		384	GlySerIleCysSerLeuSer 390		
Db		2569	GAATTCATTGTCTTCTTCTTCC 2589		
RESULT 15					
US-10-361-811-255					
Sequence 255, Application US//10361811					
Publication No. US20030206918A1					
GENERAL INFORMATION:					
APPLICANT: Fanger, Gary R.					
APPLICANT: Fling, Steven P.					
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY					
FILE REFERENCE: 210121.484C8					
CURRENT APPLICATION NUMBER: US/10/361,811					
NUMBER OF SEQ ID NOS: 293					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 255					
LENGTH: 5404					
TYPE: DNA					
ORGANISM: Homo sapiens					
US-10-361-811-255					
Alignment Scores:					
Pred. NO.: 1.59e-166 Length: 5404					
Score: 1658.50 Matches: 320					
Percent Similarity: 87.71% Conservative: 37					
Best Local Similarity: 78.62% Mismatches: 33					
Query Match: 49.95% Indels: 17					
DB: Gaps: 5					

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US-10-062-879-4 (1-636) x US-10-361-811-255 (1-5404)
OY 1 MetalAlaaglyValAlaAlaATrPLeuProPheAlaArgAlaAlaAlaIleGlyTyrMet 20
Db 1369 ATGCGCGCGGGGGGAGCGCGTGGCTCTTTTCCAAAGGCGAGCGCTATCGGGTGGATG 1428
OY 21 ProValAlaIleuAspPheMetProLeuAlaProAlaIleuAspLeuValSerGly 39
Db 1429 CCTTGGCTCTGGGGGCTTATGCCGGCTTCCCGGAGCGAGAGAGAAAGAACCCAGAT 1488
OY 40 GluLeuIleValLeuAsnValSerGlyArgArgPheGlnThrTyrArgThrThrLeuGlu 59
Db 1489 GCTCTCATTTGGCTGAATGTGAATGGAGGACCGCGCTTCCAGAGTGGCAGGACACCTGGAA 1548
OY 60 ArgTyrProArgPheThrLeuLeuGlySerThrGluValGluPhePhePheAsnGluAspThr 79
Db 1549 CGTAAACCAGACACTTCACTGAGGAGATGTGAGAGGAGACTTTTCTTCAACCCAGAAACT 1608
OY 80 LysGluIuYrPhePheAspArgAspProGluValPheArgCysValLeuAsnPheTyrArg 99
Db 1609 CAGCAGATTTCTTTGACCGTGACCGACACACTTCCGCCACATCTCGAATTTCTTACCGC 1668
OY 100 ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119
Db 1669 ACTGGGAAGCTCCACTATTCCTCGCACAGAGTGATCTCTGCTTACGATGAAGAATCGGC 1728
OY 120 PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrTyrGluGluTyrLysAspArg 139
Db 1729 TTTCTTTGGCCCTCACTCCGGAATATCATGGGACATCGTGTATATGAGAGTACAAAGATCGC 1788
OY 140 LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluValAsnGlnGluSer 159
Db 1789 AGGGAGAGAGAACCGCCGAGCGCTTCAGAGACGACCGGATACCGACACCGCTGGGGAAGC 1848
OY 160 ---MetProSerLeuSerPheArgGlnThrMetTyrAlaIlePheGluAsnProHisThr 178
Db 1849 GCCTTGCACCAATGATGTCGCAAGGAGAGGCTGTGAGAGGCGCTTCGAGAACCCCAACAC 1908
OY 179 SerThrIleuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
Db 1909 AGCAGCAGTGGCCCTGGAGTCTTACTATGATCAACGGGGTTTTCATTTGCGCTTCGTATC 1968
OY 199 ThrAsnAlaValGluThrAlaProCysGlyThrValProGlySer---LysGluLeuPro 217
Db 1969 GCGAATGTGTGAGAAACAGTGCCTGTGGGATCAAGCCCAAGTCACTTAAAGACTGCC 2028
OY 218 CysGlyGluArgTyrSerValAlaPhePheCysLeuAspThrAlaCysValMetIlePhe 237
Db 2029 TGTGGAGAGGGATATGCTGTGGCTTCTTCTGCTTGGACACGGCCTCGTCATGATCTTC 2088
OY 238 ThrValGluTyrLeuLeuArgLeuPheAlaAlaProSerArgTyrArgPheIleArgSer 257
Db 2089 ACACTTAAAGTAATTTGCTTCCCTGGCTGACAGCGCTTGTAGTACCCATTTTGGCGTAGT 2148
OY 258 ValMetSerIleIleAspValAlaAlaIleMetProTyrTyrIleGlyLeuValMetThr 277
Db 2149 GTATATGATCATCGACGTGTGGCCATCTGCTTATTTACATTTGGGCTGTATGACA 2208
OY 278 AsnAsnGluAspValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
Db 2209 GACAAATAGAGCGTCACGGAGCGCTTGTGCAACTCCGAGACTTCGGGGTCTTCAGATC 2268
OY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrThrLysSerCys 317
Db 2269 TTTTAAATTTTCCCGCACCTCTCAAGGGCTCGGACTCTCGGGGTACACATGAAAGTTGT 2328
OY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
Db 2329 GCCTCAAGATTTGGGCTTCTTGCTTTTCTCGTCAACATGGCTATCATCTTTCGTACA 2388
OY 338 ValMetPheTyrAlaGluTyrGlySerSerAlaSerLysPheThrSerIleProAlaSer 357

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QY 358 PheTPTyrrThrlleValThrMetThrThr----- 367
Db 2449 TTCTGTGATACCAATCGCACCATGACCAACCTAGGGTAGGTGCCATATATGGAAATGGGA 2508
QY 368 -----LeuGlyTyrglyAspMetVal-----ProLysThrIleValIlePhe 383
Db 2509 TGGAGCTTGGGATTTGGGTGAGGCGCATTTGTGACCCATTCAGAGTTACATGTAATCTCGGG 2568
QY 384 GlySerIleCysSerLeuSer 390
Db 2569 GAAATCATTTGTTTCTTTCC 2589

RESULT 16
US-10-369-186-255
; Sequence 255, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 5404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-255

Alignment Scores:
Pred. No.: 1,59e-166 Length: 5404
Score: 1658.50 Matches: 320
Percent Similarity: 87.71% Conservative: 37
Best Local Similarity: 78.62% Mismatches: 33
Query Match: 49.95% Indels: 17
DB: 17 Gaps: 5

US-10-062-879-4 (1-636) x US-10-369-186-255 (1-5404)
QY 1 MetAlaAlaGlyValAlaAlaATPLeuProPheAlaAlaAlaAlaIleGlyTTPMet 20
Db 1369 ATGGCGCGGGGGGGGCGAGCGGTGGCTGCTTTGGCAAGGCGACGCGTATCGGGTGAAG 1428
QY 21 ProValAlaAnCySPrometProLeuAlaProAlaAspLysAnLysArg---GlnAsp 39
Db 1429 CCTGTGGCCTCGGGGCGCTATAGCCGCTCCCGAGGCGAGAGAGAAAGACCCCAAGAT 1488
QY 40 GluLeuIleValIleuAnValSerGlyArgArgPheGlnThrTrpArgThrThrLeuGlu 59
Db 1489 GCTCTCATTTGGCTGATGATGAGTGGACCCGCTCCAGACGTTGGCAGACACCTCGGA 1548
QY 60 ArgTyrrProAspThrIleuLeuGlySerThrGluLeuGluPhePhePheAnGluAspThr 79
Db 1549 CGTTACCCAGACACTACTAGCGGCACTTCTGAGAGGGCACTTTTCTACCAACCCAGAAACT 1608
QY 80 LysGluLysPhePheAspArgAspProGluValPheArgCysValIleuAnPheTyrrArg 99
Db 1609 CACAGATATTTCTTTGACCGTACCCAGACCATCTCCGACACATCTCGAATTTCTACCCG 1668
QY 100 ThrGlyLysLeuHisTyrrProArgTyrrGluCysIleSerAlaTyrrAspAspGluLeuAla 119
Db 1669 ACTGGGAAGCTCCACTATCTCTCCGACAGATGATCTCTCTTACATGAGAACTGGCC 1728
QY 120 PheTyrglyIleLeuProGluIleIleGlyAspCysTyrrGluGluTyrrLysAspArg 139
Db 1729 TTCTTTGGCTCATCCCGGAATATCATCGGCACTGCTGTTATGAGAGTACAGATCCG 1788
QY 140 LysArgGluAnValIleGluArgLeuMetAspAspAnAspSerIleuAnGlnGlnGluSer 159
Db 1599 LysArgGluAnValIleGluArgLeuMetAspAspAnAspSerIleuAnGlnGlnGluSer 1599
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Db 1789 AGCGAGAAACGCCGAGCGCTTCAGAGACGACCGGATACCCGACACCGCTGGGAGAGC 1848
QY 160 ---MetProSerLeuSerPheArgGlnThrMetTrpArgAlaPheGluAnProHisThr 178
Db 1849 GCCTTGGCCACCAATGATGCAAGGAGGTGTGAGGGCTTCGAGAACCCCCACACC 1908
QY 179 SerThrLeuAlaLeuValPheTyrrValThrGlyPhePheIleAlaValSerValIle 198
Db 1909 AGCAGATGAGCCCTGGGTGTTTACTATATGTCAGGGGGTTTTCATATGCGCTCTGTATC 1968
QY 199 ThrAnValIleGluThrValProCysGlyThrValProGlySer---LysGluLeuPro 217
Db 1969 GCGAATGTGTGAGAAACAGTCCCGTGGGANCAGCCAGGTACATTAAGAACTGCC 2028
QY 218 CysGlyGluArgTyrrSerValAlaPhePheCysLeuAnpThrAlaCysValMetIlePhe 237
Db 2029 TGTGGAGAGCGGTATGCTGTGGCTTCTTGTGTTGACACGCGCTCGTATATCTTC 2088
QY 238 ThrValGluTyrrLeuLeuArgLeuPheAlaAlaProSerArgTyrrArgPheIleArgSer 257
Db 2089 ACAGTTGATATTTGCTTGGCTGCTGTCAGCGCTGATGCTTACCTTTTGTGGCTAGT 2148
QY 258 ValMetSerIleIleAspValAlaIleMetProTyrrTyrrIleGlyLeuValMetThr 277
Db 2149 GTCATGATATCATCGACGTGTGGCCATCTCGCTTATTCATTTGGGCTGTATGACA 2208
QY 278 AnAnGluAnpValSerGlyAlaPheValThrLeuArgValPheArgValPheArgIle 297
Db 2209 GACATGAGAGAGTCAGCGGAGCTTGTCTACACTCCAGACTCCGGGCTTCAGGATC 2268
QY 298 PheLysPheSerArgHisSerGlnGlyLeuArgIleLeuGlyTyrrThrLeuLysSerCys 317
Db 2269 TTTAAGTTTCCCGCACTTCAGAGCCCTGCGATCTCGGGAGTAACACATGAAAGATTGT 2328
QY 318 AlaSerGluLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIleIlePheAlaThr 337
Db 2329 GCCTCAGATTTGGGCTTCTTCTTCTCGTACACATGCTATCATCATCTTCGTACACA 2388
QY 338 ValMetPheTyrrAlaGluLysGlySerSerAlaSerLysPheThrSerIleProAlaSer 357
Db 2389 GTTATGTTCTACGAGAGAAAGGCTTCGCTGCTAGCAAGTTACACACATCCCTGCAGCC 2448
QY 358 PheTPTyrrThrlleValThrMetThr----- 367
Db 2449 TTCTGTATACCATGTCACATGACCAACTAGGGTAGTGCCATATGGGAAATGGGA 2508
QY 368 -----LeuGlyTyrglyAspMetVal-----ProLysThrIleValIlePhe 383
Db 2509 TGGAGCTTGGGATTTGGGTGAGGCGCATTTGTGACCCATTCAGAGTTACATGTAATCTCGGG 2568
QY 384 GlySerIleCysSerLeuSer 390
Db 2569 GAAATCATTTGTTTCTTTCC 2589

RESULT 17
US-10-029-386-24777/c
; Sequence 24777, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: ABOmica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24777
; LENGTH: 1121
; TYPE: DNA
; ORGANISM: Homo sapiens
```



	:	FEATURE INFORMATION:	MAP TO AF07550.1	
	:	OTHER INFORMATION:	EXPRESSED IN HELA, SIGNAL = 1	
	:	OTHER INFORMATION:	EXPRESSED IN PLACENTA, SIGNAL = 1.6	
	:	OTHER INFORMATION:	EXPRESSED IN LUNG, SIGNAL = 1.3	
	:	OTHER INFORMATION:	EXPRESSED IN HEART, SIGNAL = 1.9	
	:	OTHER INFORMATION:	SWISSPROT HIT: P17971, EVALUE 0.00e+00	
	:	OTHER INFORMATION:	NT HIT: g14760095, EVALUE 0.00e+00	
	:	OTHER INFORMATION:	EST_HUMAN HIT: ALI20075.1, EVALUE 0.00e+00	
	:	US-10-029-386-24777		
		Alignment Scores:		
		Pred. No.:	1.4e-149	1121
		Score:	1490.50	279
		Percent Similarity:	87.17%	Conservative: 47
		Best Local Similarity:	74.60%	Mismatches: 41
		Query Match:	44.89%	Indels: 7
		DB:	Gaps:	16 3
US-10-062-879-4	(1-636)	x US-10-029-386-24777	(1-1121)	
OY	1	MeCaLaalaglyValAlaAlaTRpleuProPhealaaValaalAllellegITrPmet	20	
Dd	1121	ATGCGCGAGCGCCTGGCCACCGTGCGCTTTGTGTCGGGAGCAGCAGCGCGCTGC	1062	
OY	21	ProVaAlaancyProMetProleuAlaProAlaapLyBaSuLyaRgJLabpLu	40	
Dd	1061	CCCCGCGCCAGCAACCCTGCGCCCGGACCCGGGGGTGAAGGCATTCTGAGAGATGAG	1002	
OY	41	LeuileVallaeAsnValSerGIYAraRgPheInTrTPargThrThreugluarG	60	
Dd	1001	GTTCTGGTGGTGAACGTGAGCGGAGCGGCTTTGAGACTTGGAGAATAACCTGGACCGC	942	
OY	61	TyrProaPhrThrleuleuglySeThrgluysgluPhepheAsnGlubspThrlys	80	
Dd	941	TACCACAGACACTTGCTGGGACGCTCGGAGAAAGAAATCTTACAGATGCATCACGAC	882	
OY	81	GluyrrPhePheaaspArgaspProgluValPheargCySvallaeasnPheTyRargThr	100	
Dd	881	GAGRACTTCTTCGANTCGGACCTGACATGTCGCCCATRGtGTAACCTTCAACGAACG	822	
OY	101	GIlylsleuHISlyrProargTyrgluCySilleseRalatyrAspAspGluleuAlaPhe	120	
Dd	821	GGGGGGCGCTGATGGCCACGGGAGAGTGCATCCAGGCTTCGACGAAGAGCTGCTTC	762	
OY	121	TyrglylleuProglullellleglyaspCySyTYrgluGuTYrLYasphArglys	140	
Dd	761	TACGGCCCTGGTCCCGAGCTAGTGCgtTAGCTGCTGCTTGAAGAATACCGGAACG	702	
OY	141	ArggluAsnAlaGluargyleuMetAspaspAsnaspsergluAsnAsnglnglusernet	160	
Dd	701	AAGAAGATGCGCAGACGCTCGGACAGAGATGACGAGGAGGACGACGCGGAGACGC--	645	
OY	161	ProSerleu-----SerPheargGlnThrmMetTrPARgalAPhegluAsnPro	176	
Dd	644	CCAAGCGCTCGCAGACGAGGAGCGCTCCGCGGACGCGCTCGGCGGGCTTGAAGATCA	585	
OY	177	HIShrSerThrleuAlaleuValPherTyrrValThrglyPhePheleAlaValSer	196	
Dd	584	CACACGAGACACCGACCGCTCGGTTTTCACTATGTGACCGGCTTCTCATCGCCGTGCG	525	
OY	197	VallleThraenValValGluThrValProcyS-----glyThrValProglYserlys	214	
Dd	524	GTCATCGCATGTGTGTGAACATCCCAATCCGCGGCTCTGCACGACGAGTCTCAAGG	465	
OY	215	GlueuProCYsglyguarGtyrSerValAlaPhePheCYsleuasPTThralaCyVal	234	
Dd	464	GAGCAGCCCTGTGGGAGAACCTTCCACAGGCGCTTTCTGATGAGACAGCCTGTSTA	405	
OY	235	MetliePheThrValGluTYrleuAsnrgleuPheAlaAlaproSerArgTYrRaphpe	254	
Dd	404	CTCATATTCACAGGGAAATACCTCTGCGCGTGTGCGGCCCCACGCGGTGCGCGTTC	345	

QY	255	11hrgrservalmetserilleilaaspvalalallemetprotyrtyrileglyleu	274
DB	344	CTGGGAGACTGCAGAGCCTCATGACGTGTGGCCATCCGCCCTACTGATGGGCTT	285
QY	275	valmettrhrnaaangluaspvalserglyalaphavalthrleuagvalpheargval	294
DB	284	TTGGTGCCCAAGAAAGCAGATGCTCTGGCCCTTTGTCACTCCGCTGTTCGGGTG	225
QY	295	phetruglilepelyspeserArXHisSerCinglyleuagllieleuglytyrThrleu	314
DB	224	TTTGCATCTTCAAGTCTCCAGGCACTCAAGGGCTTGAAGATTCTGGGCTTACACTC	165
QY	315	lysserCysalaserGluLeuglyPheleuleupheserleuthrmetalallele	334
DB	164	AAGAGCTGTGCTGTGAGCTGGGCTTCTCTCTTTTCCCAACAGGCACTATCATC	105
QY	335	PhelialthralValMetPheTyralGluLyglySerSerlaserLySpheThrSerlle	354
DB	104	TTTCCCACTGTCATGTTTATGTATGCTGAAGAGGCAAAACAGAACCACTTTACAAGATC	45
QY	355	ProbaserPheTTPYrThrIleValThrmetThrleu	368
DB	44	CTCGGCGCTTCTGTGTATACCATTTGTACATGACACAGCTT	3
RESULT 18			
US-10-212-677-256			
/ Sequence 256, Application US/10212677			
/ Publication No. US20030129192A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Chenault, Ruth A.			
/ APPLICANT: Xu, Jiangchun			
/ APPLICANT: Fanger, Gary R.			
/ APPLICANT: Harlocker, Susan L.			
/ APPLICANT: McNeill, Patricia D.			
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
/ TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER			
/ FILE REFERENCE: 210121.484C7			
/ CURRENT APPLICATION NUMBER: US/10/212, 677			
/ CURRENT FILING DATE: 2002-08-02			
/ NUMBER OF SEQ ID NOS: 288			
/ SOFTWARE: FastSeq for Windows Version 4.0			
/ SEQ ID NO 256			
/ LENGTH: 1597			
/ TYPE: DNA			
/ ORGANISM: Homo sapiens			
US-10-212-677-256			
Alignment Scores:			
Pred. No.: 1,99e-84 Length: 1597			
Score: 887.00 Matches: 161			
Percent Similarity: 90.00% Conservative: 28			
Best Local Similarity: 76.67% Mismatches: 19			
Query Match: 26.72% Indels: 2			
DB: 15 Gaps: 2			
US-10-062-879-4 (1-636) x US-10-212-677-256 (1-1597)			
QY	1	MetAlaAlaGlyValAlaAlaAlaTrpLeuProPheAlaArgAlaAlaAlaIleGlyTrpMet	20
DB	966	ATGGCGGGGGGGGGGAGCGCTGCTCTTTTGCAAGGAGGAGGCGCTATCGGGTGAATG	1025
QY	21	ProValAlaAaencySPrometProLeuAlaProAlaAspLySaenLySarg--GlnAsp	39
DB	1026	CTGTGGCTTGGGGGCTTATGCCGGCTTCCCCAGGAGCAGAGAGAAAGGACCCAGAT	1085
QY	40	GluLeuIleValLeuAaenValSerGlyAArgArpPheGlnThrTrpAgtThrThrLeuGlu	59
DB	1086	GCTCTCATTTGGCTGAATGTGAAGTGGACCCGCTTCCAGACGTGGCAGACACCCCTGAA	1145
QY	60	ArgtyrProAspThrLeuLeuGlySerThrGluLygIupPhePheAsnGluAspThr	79
DB	1146	CGTATACCAGACACTCTATCTGGGAGATTTCTGAGAGGGACTTTTCTTCAACACCCGAAACT	1205



```
QY      80  LysGluTyrPhePheAspArgProGluValPheArgCysValIleuAnpPheTyrArg  99
      1206 CAGAGATATTTCTTGAACCGGACCGACATCTTCGGACATCTCGAATTTCTACCGC  1265
QY      100  ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla  119
      1266 ACTGGGAAGCTCCACTATCTCTCGCAGAGTGCATCTCTGTTACATGAAGAAGCTGGCC  1325
QY      120  PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArg  139
      1326 TTTCTTGGCTCATCCCGGAATCATCGGACCTGTTATGAGAGATCAAGAGATCCG  1385
QY      140  LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAnGlnGlnSer  159
      1386 AGGCGAGAGAAAGCGCGAGCGCTGCAGACGACCGGATACCGACACCGCTGGGGAGAGC  1445
QY      160  ---MetProSerLeuSerPheArgGlnThreTyrArgAlaPheGluAsnProHisThr  178
      1446 GCCTTGGCCACATGACTGCAGAGGAGGAGGCTTGGAGGGCTTCGAGAAACCCCAACAC  1505
QY      179  SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle  198
      1506 AGCAGATGGCCCTGGGTCTACTATGTCACGCGGGTTTTCATGCGCTCTGTGCATC  1565
QY      199  ThrAsnValAlaGluThrValProCysGly  208
      1566 GCGAATGTGTGAAACATGTCGTCGGA  1595
DB
```

## RESULT 19

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US-10-361-811-256
; Sequence 256, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Flinn, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361.811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-256
```

## Alignment Scores:

Pred. No.:	1.99e-84	Length:	1597
Score:	887.00	Matches:	161
Percent Similarity:	90.00%	Conservative:	28
Best Local Similarity:	76.67%	Mismatches:	19
Query Match:	26.72%	Indels:	2
DB:	17	Gaps:	2

US-10-062-879-4 (1-636) x US-10-361-811-256 (1-1597)

```
QY      1  MetAlaAlaGlyValAlaAlaATrPLeuProPheAlaArgAlaAlaIleGlyTyrMet  20
      966 ATGGCGGGGGGGGGGAGCGTGCCTTTTGCAAGGCGACGGCTATCGGGTGAATG  1025
DB      21  ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg---GlnAsp  39
      1026 CCTGTGGCTCGGGGCGCTATGCGGGCTCCCGGAGGAGAGAGAAAGAACCAAGAT  1085
QY      40  GluLeuIleValIleuAsnValSerGlyArgArgPheGlnThrTyrPArgThrThrLeuGlu  59
      1086 GCTCTCATTTGCTGAATGTGAGTGACACCGCTTCAGACGTGGCAGACACCCCTGGAA  1145
DB      60  ArgTyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThr  79
      1146 CGTATCCAGACACTTACTGAGGAGTTCTGAGAGGAACTTTTCTACCAACCAAGAACT  1205
DB
```

```
QY      80  LysGluTyrPhePheAspArgProGluValPheArgCysValIleuAnpPheTyrArg  99
      1206 CAGAGATATTTCTTGAACCGGACCGACATCTTCGGACATCTCGAATTTCTACCGC  1265
QY      100  ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla  119
      1266 ACTGGGAAGCTCCACTATCTCTCGCAGAGTGCATCTCTGTTACATGAAGAAGCTGGCC  1325
QY      120  PheTyrGlyIleLeuProGluIleIleGlyAspCysTyrGluGluTyrLysAspArg  139
      1326 TTTCTTGGCTCATCCCGGAATCATCGGACCTGTTATGAGAGATCAAGAGATCCG  1385
QY      140  LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAnGlnGlnSer  159
      1386 AGGCGAGAGAAAGCGCGAGCGCTGCAGACGACCGGATACCGACACCGCTGGGGAGAGC  1445
QY      160  ---MetProSerLeuSerPheArgGlnThreTyrArgAlaPheGluAsnProHisThr  178
      1446 GCCTTGGCCACATGACTGCAGAGGAGGAGGCTTGGAGGGCTTCGAGAAACCCCAACAC  1505
QY      179  SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle  198
      1506 AGCAGATGGCCCTGGGTCTACTATGTCACGCGGGTTTTCATGCGCTCTGTGCATC  1565
QY      199  ThrAsnValAlaGluThrValProCysGly  208
      1566 GCGAATGTGTGAAACATGTCGTCGGA  1595
DB
```

## RESULT 20

```
US-10-369-186-256
; Sequence 256, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Flinn, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369.186
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-369-186-256
```

## Alignment Scores:

Pred. No.:	1.99e-84	Length:	1597
Score:	887.00	Matches:	161
Percent Similarity:	90.00%	Conservative:	28
Best Local Similarity:	76.67%	Mismatches:	19
Query Match:	26.72%	Indels:	2
DB:	17	Gaps:	2

US-10-062-879-4 (1-636) x US-10-369-186-256 (1-1597)

```
QY      1  MetAlaAlaGlyValAlaAlaATrPLeuProPheAlaArgAlaAlaIleGlyTyrMet  20
      966 ATGGCGGGGGGGGGGAGCGTGCCTTTTGCAAGGCGACGGCTATCGGGTGAATG  1025
DB      21  ProValAlaAsnCysProMetProLeuAlaProAlaAspLysAsnLysArg---GlnAsp  39
      1026 CCTGTGGCTCGGGGCGCTATGCGGGCTCCCGGAGGAGAGAGAAAGAACCAAGAT  1085
QY      40  GluLeuIleValIleuAsnValSerGlyArgArgPheGlnThrTyrPArgThrThrLeuGlu  59
      1086 GCTCTCATTTGCTGAATGTGAGTGACACCGCTTCAGACGTGGCAGACACCCCTGGAA  1145
DB      60  ArgTyrProAspThrLeuLeuGlySerThrGluLysGluPhePheAsnGluAspThr  79
      1146 CGTATCCAGACACTTACTGAGGAGTTCTGAGAGGAACTTTTCTACCAACCAAGAACT  1205
DB
```

```
Db      1146 CGTACCAGACACTCTACTGCGAGTTCTGAGAGGAGCTTTTCTACCAACCAAACT 1205
Qy      80  LysGluTyrPhePheAspArgAspProGluValPheArgCysValIleuAsnPheTyrArg 99
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     1206 CAGCAGATTTCTTTGACCGGACCGACACATCTTCGCCACATCCTGAATTTCTACCGC 1265
Qy     100  ThrGlyLysLeuHisTyrProArgTyrGluCysIleSerAlaTyrAspAspGluLeuAla 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     1266 ACTGGAGAAGCTCCACTATCCTCGCCACAGATGCAATCTCTGCTTACGATGAAGAAGTGGCC 1325
Qy     120  PheTyrGlyIleLeuProGluIleIleGlyAspCysCysTyrGluGluTyrLysAspArg 139
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     1326 TTCTTTGCGCTCATCCCGAAATCATCGCGCATGCTGTATGAGAGATACAGGATCGC 1385
Qy     140  LysArgGluAsnAlaGluArgLeuMetAspAspAsnAspSerGluAsnAsnGlnGluSer 159
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     1386 AGGCGAGAGAAAGCGGAGCGCTTCAGAGACGACCGGATACCGACCGCTGGGGAGAGCC 1445
Qy     160  ---MetProSerLeuSerPheArgGlnThrMetTyrArgAlaPheGluAsnProHisThr 178
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     1446 GCCTTGCCCAACGATGACGAGGAGGAGGTCTGAGAGGCGCTTCGAGAACCCCAACACC 1505
Qy     179  SerThrLeuAlaLeuValPheTyrTyrValThrGlyPhePheIleAlaValSerValIle 198
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     1506 AGCAGCATGGCGCTGTGTCTACTATGTCAAGGGGTTTTTCATGCGCGTCTGTGCATC 1565
Qy     199  ThrAsnValValGluThrValProCysGly 208
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     1566 GCGAATGTGTGAAACAGTCCGTGCGGA 1595
```

Search completed: April 13, 2005, 22:49:10  
Job time : 882.439 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 13, 2005, 11:52:53 ; Search time 4396.82 Seconds  
(without alignments)  
5505.991 Million cell updates/sec

Title: US-10-062-879-4  
Perfect score: 3320  
Sequence: 1 MAAGVAAWLPARAAAIAGMM.....PCPNTNIPSITSNVKVSVL 636

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+g2n.model -DEV=xlp  
-O=/cgn2.1/USPTO\_spool\_P/US10062879/runcat\_12042005\_113502\_16932/app\_query.fasta\_1.1614  
-DB=EST -QFMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0 -LIST=45  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIT=45  
-DOCLIN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL  
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10062879@cgn\_1\_1\_6628@runcat\_12042005\_113502\_16932 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6  
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gse1:\*  
9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3311	99.7	1911	9	AY419307 Homo sapi
2	3398	99.3	1911	9	AY419309 Mus muscu
3	3123	94.1	1911	9	AY419308 Pan trogl
4	2544.5	76.6	3730	3	AK031962 Mus muscu
5	2523	76.0	2997	3	AK032268 Mus muscu
6	2407	72.5	1893	9	AY406814 Mus muscu
7	2399	72.3	1893	9	AY406812 Homo sapi
8	2141.5	64.5	1956	9	AY408065 Mus muscu
9	2132.5	64.2	1944	9	AY408063 Homo sapi

10	1701	51.2	1893	9	AY406813 Pan trogl
11	1626.5	49.0	1939	9	AY408064 Pan trogl
12	1551.5	46.7	3302	3	AK031805 Mus muscu
13	1317.5	39.7	1054	9	CNS03211 Tetraodon
14	1270.5	38.3	993	9	CNS0590A Tetraodon
15	1209.5	36.4	997	9	CNS02DRX Tetraodon
16	1073.5	32.3	857	5	BU411177 B2203918
17	1033	31.1	628	8	BZ203918 CH230-390
18	1018.5	30.7	723	7	CO393575 AGENCOURT
19	988.5	29.8	753	7	CN220459 RJAO66409
20	988	29.8	695	1	AL120075 DKFZP761M
21	950.5	28.6	647	7	CE500559 tigr-gsa-
22	916	27.6	636	7	CF897059 A0219E07-
23	915.5	27.6	698	5	BM47382 UI-M-EGDP
24	898.5	27.1	956	6	CA477676 AGENCOURT
25	891	26.8	903	9	CNS02SAE Tetraodon
26	885	26.7	600	7	CR548281 DKFZP459P
27	840	25.3	715	6	CB167795 FBB60300
28	837	25.2	662	9	CE336550 tigr-gsa-
29	817	24.6	576	8	AZ49487 IM0247E16
30	816.5	24.6	567	4	BT033106 MR4-NN020
31	815.5	24.6	647	2	BB625540 BB625540
32	798.5	24.1	594	5	BP209965 BP209965
33	755.5	22.8	814	7	CF530818 UI-M-GHO-
34	753	22.7	2565	9	AY417318 Homo sapi
35	748.5	22.5	477	7	CR790592 DKFZP459M
36	747	22.5	796	5	BU342672 BU3519328
37	745	22.4	463	6	CD804043 UI-M-GVO-
38	736.5	22.2	595	7	CR540971 DKFZP459A
39	728	21.9	679	2	BB625814 BB625814
40	725.5	21.9	2562	9	AY417320 Mus muscu
41	719	21.7	1572	9	AY400869 Homo sapi
42	718.5	21.6	1758	9	AY398826 Homo sapi
43	717.5	21.6	1758	9	AY398828 Mus muscu
44	716.5	21.6	1587	9	AY400871 Mus muscu
45	713.5	21.5	1488	9	AY412413 Homo sapi

## ALIGNMENTS

RESULT 1	AY419307	1911 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY419307				
DEFINITION	Homo sapiens KCND3 gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY419307				
VERSION	AY419307.1	GI:39775264			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1911) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Interfing nonneutral evolution from human-chimp-mouse orthologous gene trices				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1911) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
AUTHORS	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..1911				



RESULT 2  
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LOCUS Mus musculus KCND3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY419309  
VERSION AY419309.1 GI:39775266  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
AUTHORS 2 (bases 1 to 1911)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering  
them based on alignment.  
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QY 301 SerArgHisSerGlnGlyLeuAargIleLeuGlyTyrThrLeuLysSerCysAlaSerGlu 320  
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QY 461 GluGluGluHisMetGlyLysThrThrSerLeuIleGluSerGlnHisHisLeuLeu 480  
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Db	1501	TGCATGAGAGAGCTCGATCAGAACTACCCCTCCACCAAGATGCTTCTCTCCAGCAC	1560
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Db	1561	TGGGCGCTCACCACTGCTGCTCCCTGCTGACAAAGAACCAACACTGCCCCAAC	1620
QY	541	SerAenLeuProAlaThArArgLeuArgSerMetGlnGluLeuSerThHisIleGln	560
Db	1621	TCTAACCTGCGCGCCACCGCGCTGGCAGATGACGAGAGCTCAGACGCTCCATCCAG	1680
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QY	601	ProProAlaLeuThProGluGlyGluSerArgProProProAlaSerProGlyProasn	620
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LOCUS			linear
DEFINITION	Pan troglodytes KCND3 gene, VIRUAL TRANSCRIPT, partial sequence,		GSS 17-DEC-2003
ACCESSION	AY419308		
VERSION	AY419308.1	GI:39775265	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Pan troglodytes		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		
	1 (bases 1 to 1911)		
	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,		
	Todd,M.A., Tenebaum,D.M., Civiello,D.R., Lu,F., Murphy,B.,		
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		
	Adams,M.D. and Cargill,M.		
TITLE	Interfing nonneutral evolution from human-chimp-mouse orthologous		
JOURNAL	gene cltos		
PUBMED	Science 302 (5652), 1960-1963 (2003)		
REFERENCE	14671302		
AUTHORS	2 (bases 1 to 1911)		
	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,		
	Todd,M.A., Tenebaum,D.M., Civiello,D.R., Lu,F., Murphy,B.,		
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		
	Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,		
COMMENT	Rockville, MD 20850, USA		
	These sequences were made by sequencing genomic exons and ordering		
	them based on alignment.		
FEATURES	Location/Qualifiers		
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Carninci, P. and Hayashizaki, Y.	
TITLE	High-efficiency full-length cDNA cloning	
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE	99279253	
PUBMED	10349636	
REFERENCE		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	
MEDLINE	20499374	
PUBMED	11042159	
REFERENCE		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, N., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Obara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer	
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE	20530913	
PUBMED	11076861	
REFERENCE		
AUTHORS		
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
JOURNAL	Functional annotation of a full-length mouse cDNA collection	
REFERENCE	Nature 409, 685-690 (2001)	
AUTHORS		
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
REFERENCE	Nature 420, 563-573 (2002)	
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imochani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanakawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sato, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.	



FEATURES  
SOURCE

Location/Qualifiers  
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## ORIGIN

## Alignment Scores:

Pred. No.: 4.77e-229 Length: 3730  
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Best Local Similarity: 86.17% Mismatches: 42  
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US-10-062-879-4 (1-636) x AK033962 (1-3730)

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AUTHORS	Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.			
TITLE	Carninci, P. and Hayashizaki, Y.			
JOURNAL	High-efficiency full-length cDNA cloning			
MEDLINE	Mech. Enzymol. 303, 19-44 (1999)			
PUBMED	99279253			
REFERENCE	10349636			
AUTHORS	2			
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,			
JOURNAL	Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
MEDLINE	Normalization and subtraction of cap-trapper-selected cDNAs to			
PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes			
REFERENCE	Genome Res. 10 (10), 1617-1630 (2000)			
AUTHORS	3			
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,			
JOURNAL	Kono, H., Akiyama, J., Nishi, K., Kitsuaki, T., Tashiro, H., Itoh, M.,			
MEDLINE	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,			
PUBMED	Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, Y.,			
REFERENCE	Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,			
AUTHORS	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,			
TITLE	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format			
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)			
PUBMED	20530913			
REFERENCE	11076861			
AUTHORS	4			
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the			
JOURNAL	FANTOM Consortium.			
MEDLINE	Functional annotation of a full-length mouse cDNA collection			
PUBMED	Nature 409, 685-690 (2001)			
REFERENCE	5			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research			
TITLE	Group Phase I & II Team.			
JOURNAL	Analysis of the mouse transcriptome based on functional annotation			
MEDLINE	of 60,770 full-length cDNAs			
PUBMED	Nature 420, 563-573 (2002)			
REFERENCE	6 (bases 1 to 2997)			
AUTHORS	Adachi, S., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,			
TITLE	Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,			
JOURNAL	Hayashida, K., Hayatsu, N., Hizomoto, K., Hiraoka, T., Hirozane, T.,			
MEDLINE	Hoti, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,			
PUBMED	Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,			
REFERENCE				

TITLE  
JOURNAL

COMMENT  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Explotation Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>  
Fax: 81-45-503-9216

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ORIGIN

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US-10-062-879-4 (1-636) x AK032268 (1-2997)

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 REFERENCE 1 (bases 1 to 1893)  
 Clark,A.G., Gianoweki,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenduum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.C.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302

REFERENCE 2 (bases 1 to 1893)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
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 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
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QY 616 SerProgluProaenThrAnlleProSerIleThrSerAnValValylsValSerVal 635  
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QY 636 leu 636  
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LOCUS Homo sapiens KCND2 gene, VIRUTAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY406812  
VERSION AY406812.1 GI:39762783  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1893)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1893)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
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 1 (bases 1 to 1956)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.O., Sniatsky,J.O.,  
 Adams,M.D. and Cargill,M.  
 TITLE inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1956)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.O., Sniatsky,J.O.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
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 VERSION AY408063.1 GI:39764034  
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 REFERENCE  
 1 (bases 1 to 1944)  
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Interfing nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
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 2 (bases 1 to 1944)  
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
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 Adams,M.D. and Cargill,M.  
 Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
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 This sequence was made by sequencing genomic exons and ordering  
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 Qy 1 MetAlaIleGlyValAlaIleAlaIleThrLeuProPheAlaArgAlaIleIleGlyYrThrMet 20







Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL  
 Science 302 (5652), 1960-1963 (2003)  
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 AUTHORS  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
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 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 REFERENCE 1 (bases 1 to 1939)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Interfering nonneutral evolution from human-chimp-mouse orthologous  
 gene trilos  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 REFERENCE 2 (bases 1 to 1939)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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**ATTORNS** Carninci, P. and Hayashizaki, Y.  
**TITLE** High-efficiency full-length cDNA cloning  
**JOURNAL** Meth. Enzymol. 303, 19-44 (1999)  
**MEDLINE** 99279253  
**PUBMED** 10349636  
**REFERENCE** 2  
**ATTORNS** Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
**TITLE** Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
**JOURNAL** Normalization and subtraction of cap-trapper-selected cDNAs to  
**MEDLINE** prepare full-length cDNA libraries for rapid discovery of new genes  
**PUBMED** Genome Res. 10 (10), 1617-1630 (2000)  
**REFERENCE** 20499374  
**ATTORNS** 11042159  
**REFERENCE** 3  
**ATTORNS** Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,  
**TITLE** Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,  
**JOURNAL** Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
**MEDLINE** Yamamoto, R., Matsumoto, H., Sakaue, S., Ikegami, T., Kashiwagi, K.,  
**PUBMED** Fujikawa, S., Inoue, K., Togawa, Y., Iwaw, M., Ohara, E., Matsubara, S., Kawai, J.,  
**REFERENCE** Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
**ATTORNS** Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
**TITLE** RIKEN integrated sequence analysis (RISA) system-384-Format  
**JOURNAL** sequencing pipeline with 384 multicapillary sequencer  
**MEDLINE** Genome Res. 10 (11), 1757-1771 (2000)  
**PUBMED** 20530913  
**REFERENCE** 11076861  
**ATTORNS** 4  
**REFERENCE** The RIKEN Genome Exploration Research Group Phase II Team and the  
**ATTORNS** PANTOM Consortium.  
**TITLE** Functional annotation of a full-length mouse cDNA collection  
**JOURNAL** Nature 409, 685-690 (2001)  
**REFERENCE** 5  
**ATTORNS** The PANTOM Consortium and the RIKEN Genome Exploration Research  
**TITLE** Group Phase I & II Team.  
**JOURNAL** Analysis of the mouse transcriptome based on functional annotation  
**REFERENCE** of 60,770 full-length cDNAs  
**ATTORNS** Nature 420, 563-573 (2002)  
**REFERENCE** 6 (bases 1 to 3302)  
**ATTORNS** Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
**TITLE** Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,  
**JOURNAL** Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
**REFERENCE** Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
**ATTORNS** Katoh, H., Kawai, T., Kojima, Y., Kondo, S., Konno, H., Konda, M.,  
**TITLE** Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
**JOURNAL** Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Onose, N.,  
**REFERENCE** Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N.,  
**ATTORNS** Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,  
**TITLE** Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
**JOURNAL** Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yaeunishi, A.,  
**REFERENCE** Muramatsu, M. and Hayashizaki, Y.  
**ATTORNS** Direct Subdivision  
**TITLE** Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
**JOURNAL** Physical and Chemical Research (RIKEN), Laboratory for Genome  
**REFERENCE** Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
**ATTORNS** RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama  
**TITLE** Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,  
**JOURNAL** URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
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LOCUS

DEFINITION

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070F19 of library G from Tetraodon nigroviridis, genomic survey

ACCESSION

AL267651

VERSION

AL267651.1

GI:7989467



TITLE	Saurin, M., Bernot, A. and Weissenbach, J.
JOURNAL	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
MEDLINE	Genome Res. 10 (7), 939-949 (2000)
PUBMED	20359837
REFERENCE	10899143
AUTHORS	3 (bases 1 to 993)
TITLE	Genoscope.
JOURNAL	Direct Submission
COMMENT	Submitted (12-Apr-2000) Genoscope - Centre National de Sequençage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .
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Oy	151 AsnAspSerGluAsnAsnGlnGluSerMetProSerLeuSerPheArgGlnThrMetTrp 170
Dd	748 CAGGAG--GAGAAACAAAGACCAAGAGCTCCCCAACATGACATTCAAGCGACGACATGTGG 692
Oy	171 ArgAlaPheGluAsnProHietHrsSerThrLeuAlaLeuValPheTyrrTyrrValThngly 190
Dd	691 CGCGCTTTGAGAACCCCAACACCTTCACATGAGCCCTGGTCTTCTATTAACGTCAAGGT 632
Oy	191 PhePheIleAlaValSerValIleThrAsnValValGluThrValProCysglYthrVal 210
Dd	631 TTCTTCATCGGCATGTGGGTATCAACAAACGTGGTGGAGAGCGGTGC-TGGGATTCTAG 573
Oy	211 ProGlySerTyrgLueuProCysglYguArgTyrrSerValAlaPhePheCysAleuAsp 230
Dd	572 GCCAATGAGAAAGACGTCCGTGTGAAGCGCTACACGTTGCGTCTTCTTCGACATGAC 513
Oy	231 ThrAlaCysValMetIlePheThrValGluTyrrLeuLeuArgLeuPheAlaIalProser 250
Dd	512 ACGGCTCTGGATATATCTTCACTGAGATGACTGATGCGGCTGTTCGCCCGCGCTACG 453
Oy	251 ArgTyrrArgPheIleArgSerValMetSerIleIleAspValValAlaIleMetProTyrr 270

Db	452	CGTTACCGCTTATGCGCCTCGGTGATAGCATCATTTGACGTGATGGCCATCTGCCTTAC	393
Oy	271	TyrlllelglyLeuValMetThrAsnAsnGluAspValSerGlyAlaPheValThrLeuArg	250
Db	392	TACATTGGCTTGATGATGCCAACAAACAAGGACGTGACGGCGCTTCGN-TMCMTGGCG	334
Oy	291	ValPheArGValPheAraGllIlePheLysPheSerArgHisSerGlnGlyLeuArgIleLeu	310
Db	333	GTCCTTCGGCGCTTCGCAATCTTCMAAGTTCTCCCGCACCTGCAGGGCGCTGGCATCTTG	274
Oy	311	GlyYTrhThreuleuYsserCyalaSerGluLeuGlylPheLeuLeuPheSerLeuThMet	330
Db	273	GGCTACACGCTCAAAG-TGGCGCTCGGAGCTGGGCTTCTCGCTCTTCCTTCACCATG	215
Oy	331	AlallellellePhealathrvalMetPheTyrrAlaGluLysGlySerSeraAlaSerLys	350
Db	214	GCCATCATCATCTTCGCCACCGTCATGTTCTACGCGAGAAGAGATCACCTCCAGCAAG	155
Oy	351	PheHrserIlePcoAlaSerPheTrpTYrThrIleValThrmethTrhThrLeuGly	369
Db	154	TTTACCAGATACCCGGCTTCCTTCGTGTACATAATTGTGACTATGACAAACATGGGG	98
<b>RESULT 15</b>			
CNS02DRX/c	LOCUS	CNS02DRX	997 bp DNA linear GSS 01-SEP-2000
DEFINITION	Tetradodon nigroviridis genome survey sequence PUC-Ori end of clone 26N04 of library G from Tetradodon nigroviridis, genomic survey sequence.		
ACCESSION	ALJ92822.1 GI:7830926		
VERSION	GSS; genome survey sequence.		
KEYWORDS	Tetradodon nigroviridis		
SOURCE	Tetradodon nigroviridis		
ORGANISM	Eukaryota; Metazoa; Chordata; Granaia; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetradodon.		
REFERENCE	1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzmes,C., Wincker,P., Broctier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)		
JOURNAL	MEDLINE 20296633		
PUBMED	10835645		
REFERENCE	2 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costez,C., Fitzmes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)		
AUTHORS	3 (bases 1 to 997) Genoscope.		
TITLE	Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.		
JOURNAL	MEDLINE 10899143		
PUBMED	20359637		
REFERENCE	3 (bases 1 to 997) Genoscope.		
AUTHORS	Location/Qualifiers		
TITLE	1..997		
JOURNAL	FEATURES		
SOURCE	/organism="Tetradodon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone="26N04" /clone_id="G"		





```

Db      183 CTCGAGCTGACGGATCCAGTCAAGATGAAACAGATACGACTMAAGGCACTCTTAATT 242
Qy      473 G|USeRg|InH|e|H|e|St|e|u|e|u|H|S|C|y|S|e|u|g|U|u|y|Th|Th|----- 487
Db      243 GAAAGCACAATACACCACTGCTGACCTGCTGAAAGAAACCGAGATTGCTTATCTT 302
Qy      488 -----Asn|Sg|U|P|H|e|I|e|A|P|----- 493
Db      303 GTGATGATCCCTGTATCTGTAGAACTTCACCATCAAGAACACAGAGTTCAATAGT 362
Qy      494 G|U|g|In|Me|t|P|H|e|g|U|In|g|In|S|C|y|Me|t|U|Se|R|e|t|G|In|S|T|Y|P|ro|Se|Th|A|g| 513
Db      363 GAGCAACTGTTTCAGACAGAACTGACATGAGAGCTCAATGCAAACTACCCGCTTCTCCG 422
Qy      514 SerProSerLeuSerSerHisProglYleuThrThrThrCysCysSerArgArgSerIys 533
Db      423 AGCCCTCTCTGTCAAGTCAACACGCGCTGACACCTCTGCTGTTCTTCGCGTCAAG 482
Qy      534 LysThrThrHisLeuProAsnSerAsnLeuProAlaThrArgLeuArgSerMetGlnIu 553
Db      483 AAGACCAACACACTTCCCACTCCAGCGCTCAGCTACCCGCTCCGACGATGACAGAG 542
Qy      554 LeuSerThrThrHisIleGlnIleYserGlnIleProSerLeuThrThrSerArgSerSer 573
Db      543 CTCAGACCATCATCATCATGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 602
Qy      574 LeuAlaLeuYsAlaAspAspGlyLeuLysProAlaProAlaCysYsYsThrSerGlnIleThrThr 593
Db      603 CTCACATCAATCAATCAATGATGAGTGGCTGCACCACTGCAAGAGAGAGAGAGAGAG 662
Qy      594 AlaIleIleSerIleProThrProProAlaLeuThrProGlnIleGlnIleSerArgProPro 613
Db      663 GCCATCATCAAGATCCCACTCCAGCGCTCAGCTCAGCAACCAAGAGAGAGAGAGAG 722
Qy      614 ProAlaSerProGlyProAsnThrAsnIle---ProSerIleThrSerAsnValValIy 632
Db      723 CCCAGCAGCGCGCGGCACTCCAGCAAACTTTCTACACCAACCAAGCAACATGTGA 782
Qy      632 sValSerValLeu 636
Db      783 GGTCTCTGCTTG 795

RESULT 17
LOCUS      BZ203918          628 bp      DNA      linear      GSS 11-OCT-2002
DEFINITION CH230-390G12.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
ACCESSION  BZ203918
VERSION    BZ203918.1  GI:23861970
KEYWORDS   GSS.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 628)
            Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
            Rat BAC End Sequences from Library CHORI-230 Mbol segment
            Unpublished (1999)
            Other GSS: CH230-390G12.TU
COMMENT    Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pjejong@mail.cno.org).
            Clones may be purchased from BACPAC Resources

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(http://www.chori.org/bacpac/or ering_information.htm) . BAC end
page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
Plate: 390 row: G column: 12
Seq primer: 17
Class: BAC end.
FEATURES             location/Qualifiers
     source           1..628
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCM"
                     /db_xref="taxon:10116"
                     /clone="CH230-390G12"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_id="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol;
                     CHORI-230 Rat (BN/SsNHsd/MCM) BAC library produced by
                     Pieter de Jong"

ORIGIN
Alignment Scores:
Pred. No.:          3,74e-87          Length:          628
Score:              1033.00           Matches:          203
Percent Similarity: 98.09%            Conservative:    2
Best Local Similarity: 97.13%          Mismatches:     4
Query Match:        31.11%             Indels:          1
DB:                  8                 Gaps:            0

US-10-062-879-4 (1-636) x BZ203918 (1-628)

Qy      129 G|Y|A|P|C|y|S|C|y|T|Y|G|U|G|U|T|Y|L|y|S|A|P|A|g|Y|S|A|g|U|A|S|n|A|g|U|A|g|U|e|u|Met 148
Db      2   GCGCACTCTCTGATGAGAGATGACAAATAC -CGCAAGCGGAGAGACGTGAGCGGCTCATG 60
Qy      149 A|S|P|A|S|A|S|P|S|e|G|U|A|S|A|S|n|I|n|g|U|S|e|t|P|ro|S|e|R|e|u|S|e|P|H|e|A|g|I|n|Th|r 168
Db      61  GATGACATGAGTCTGAGAAACAACAGAGATGCATGCCCTCCCTGAGCTTCCTACATGCG 120
Qy      169 M|e|t|T|P|A|g|A|A|P|H|e|g|U|A|S|P|ro|H|e|Th|S|e|R|Th|L|e|u|A|I|e|u|A|P|H|e|T|Y|T|Y|T|Val 188
Db      121 A|T|G|G|C|G|G|G|C|T|T|G|A|A|C|C|A|C|A|C|A|C|G|A|C|C|T|G|G|A|C|T|G|T|T|C|T|A|C|A|G|G 180
Qy      189 T|H|g|Y|P|H|e|I|e|A|I|V|A|S|e|R|V|A|I|e|Th|A|S|n|V|A|I|G|U|Th|V|A|P|ro|C|y|S|g|Y 208
Db      181 A|C|A|G|C|T|T|C|T|A|T|T|G|C|G|G|T|C|T|G|G|T|A|T|C|A|C|A|C|G|T|G|G|A|C|G|G|T|C|A|G|C|G|G|C 240
Qy      209 T|H|V|A|P|ro|G|Y|S|e|T|Y|S|e|U|P|ro|C|y|S|g|Y|U|A|g|Y|T|Y|S|e|V|A|I|A|P|H|e|B|e|C|y|S 228
Db      241 A|C|G|G|C|T|G|G|G|A|G|A|A|G|A|A|C|T|G|C|G|T|G|A|G|A|G|G|C|T|A|C|T|C|G|G|C|T|T|T|G|C 300
Qy      229 L|e|u|A|P|Th|A|I|C|y|S|V|A|I|e|t|I|e|P|H|e|Th|V|A|I|G|U|T|Y|L|e|u|L|e|u|A|g|U|e|u|P|H|e|A|I|A 248
Db      301 C|T|G|A|C|A|C|T|G|G|G|T|G|T|A|T|G|A|T|T|C|A|C|G|T|G|A|G|T|A|C|T|C|C|G|A|C|T|T|C|C|G|G|C|A 360
Qy      249 P|ro|S|e|R|A|g|Y|T|A|S|P|H|e|I|A|S|e|R|V|A|I|e|t|S|e|R|I|e|I|e|A|S|P|V|A|I|A|I|e|Met 268
Db      361 C|C|A|G|A|C|A|G|T|A|C|G|T|T|A|T|C|G|A|G|T|G|A|T|G|A|C|A|T|C|A|G|A|C|G|T|G|C|A|T|C|A|G 420
Qy      269 P|ro|T|Y|T|I|e|G|Y|L|e|u|V|A|I|e|t|H|z|A|S|n|A|S|n|I|e|A|P|V|A|I|S|e|G|Y|A|I|A|P|H|e|V|A|I|Th|r 288
Db      421 C|C|C|A|T|T|A|C|A|T|T|G|G|C|T|G|T|A|T|G|A|C|A|A|C|A|G|A|G|A|G|G|G|G|G|C|A|T|T|T|G|T|C|A 480
Qy      289 L|e|u|A|g|V|A|I|P|H|e|A|g|V|A|I|P|H|e|Y|S|P|H|e|S|e|A|T|G|H|I|S|e|R|G|I|N|G|Y|L|e|u|A|g 308
Db      481 C|T|C|G|G|G|T|T|C|C|G|G|T|T|C|A|G|A|T|T|T|C|A|A|G|T|T|C|C|A|C|A|T|T|C|C|A|G|G|G|C|T|A|G|G 540
Qy      309 I|l|e|u|G|Y|T|Th|L|e|u|Y|S|e|C|y|S|A|S|e|R|G|U|e|u|G|Y|P|H|e|L|e|u|P|H|e|S|e|R|e|u 328
Db      541 A|T|C|T|A|G|C|T|A|C|C|C|T|A|A|A|G|C|T|G|G|C|T|C|A|A|A|C|T|A|G|G|C|T|T|C|T|C|T|C|C|C|T|C 600
Qy      329 T|H|M|e|t|A|I|e|I|e|I|e|P|H|e|A|I|Th|r 337
Db      601 A|C|A|T|G|G|G|A|C|A|T|C|A|T|C|T|T|G|C|C|A|C|T 627

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RESULT 18  
 CO393575 723 bp mRNA linear EST 01-JUL-2004  
 LOCUS AGNCOURT 26755085 NIH MGC 255 Rattus norvegicus cDNA clone  
 DEFINITION IMAGE:7321104 5', mRNA sequence.  
 CO393575  
 ACCESSION CO393575.1 GI:49575491  
 VERSION EST.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 723)  
 REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Daniela S. Gerhard, Ph.D.  
 COMMENT Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgsrbs-remail.nih.gov  
 Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical  
 College of Wisconsin  
 cDNA Library Preparation: Express Genomics  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: LHAM15384 Row: G Column: 22  
 High quality sequence stop: 690.  
 Location/Qualifiers

## FEATURES

source

1..723  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="IMAGE:7321104"  
 /sex="both"  
 /tissue\_type="Brain - Pooled from several tissues from one  
 or more individuals"  
 /lab\_host="DH10B Toba"  
 /clone\_lib="NIH\_MGC\_255"  
 /note="Organ: brain/CNS; Vector: pExpress-1; Site: 1:  
 EcoRV; Site 2: NotI; RNA obtained from brain tissue of 8  
 wk old animal. Tissues were snap-frozen and kept at -80C  
 before RNA extraction and purification (Tri-reagent  
 method). cDNA was primed using oligo-dT primer:  
 5'-pGACGAGTCTAGATCGGAGCGCCGCC(T)25-3' and cloned into  
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb  
 resulted in an average insert size of 1.7 kb. This primary  
 library is a normalized (primary library is NIH MGC 254)  
 and was constructed by Express Genomics (Frederick, MD).  
 Note: this is a NIH\_MGC library"

## ORIGIN

## Alignment Scores:

Pred. No.: 1..85 Length: 723  
 Score: 1018.50 Matches: 199  
 Percent Similarity: 90.04% Conservative: 18  
 Best Local Similarity: 82.57% Mismatches: 23  
 Query Match: 30.68% Indels: 1  
 DB: 7 Gaps: 1

US-10-062-879-4 (1-636) x CO393575 (1-723)

QY 294 ValPheArgIlePheIlePheSerArgHisSerGlnGlyLeuArgIleGlyTyrThr 313  
 Db 3 GTCTTCAGAGATCTTAAAGTTTCCCGCACCTCAAGCGCTGCTATATCGGGATACACA 62  
 QY 314 LeuIysSerGlyAlaSerGlnLeuGlyPheLeuLeuPheSerLeuThrMetAlaIleIle 333

Db 63 CTGAAGAGCTGCGCTCAGAACTGGGCTTCTTGCTTTCCCTCACAATGCTATCATC 122  
 QY 334 IlePheAlaThrValMetPheTyrAlaGluIysGlySerSerAlaSerIysPheThrSer 353  
 Db 123 ATTTTCGATCAGCGTATGTTTCTACCGCAGAGAGGCTCTTACAGCAAGCAATTCACCGC 182  
 QY 354 IleProAlaSerPheThrPyrThrIleValThrMetThrLeuGlyTyrGlyAspMet 373  
 Db 183 ATCCCTGACGCTTGTGTACACATGCTCACACATGACACACATGGGTATGGGACATG 242  
 QY 374 ValProIysThrIleAlaGlyIlePheGlySerIleCysSerLeuSerGlyValIleu 393  
 Db 243 GTCACCAAAACCATGACGAGGAAAGTTTCGGGTATCTCTCTCTGAGCGAGATCTTG 302  
 QY 394 ValIleAlaLeuProValProValIleValSerAnPheSerArgIleTyrHisGlnAsn 413  
 Db 303 GTCATCGCGCTACCGCTGCTGTGATCGTCTTAATTCAGTCGATCTACCAACCAAC 362  
 QY 414 GlnArgAlaAspIysArgArgAlaGlnIleIysAlaArgLeuAlaArgValAla 433  
 Db 363 CACAGAGCGGACAAACGAGGACACAGAAAGGAGGCTGGCCAGGATCCGGACAGCC 422  
 QY 434 LysThrGlySerSerAsnAlaTyrLeuHisSerIysArgAnGlyLeuLeuAsnGluAla 453  
 Db 423 AAAAGTGAAGTGCATAATGCTTACATGACAGCAAGCGAATGGTTACTAGACACCA 482  
 QY 454 LeuGluLeuThrGlyThrProGluGluGluHisMetGlyIysThrThrSerLeuIleGlu 473  
 Db 483 CTGCAG--TCTCGAGAGATGAACCGGCTTCTGTTAGCAATCTGATCGATCGTTCGAG 539  
 QY 474 SerGlnHisIleHisLeuLeuHisCysLeuGlnIlyThrThrAnHisGluPheIleAsp 493  
 Db 540 AACACACACACACACCTCTCTCAGCTGAGGAAACACGAAACCAAGCACTTGTGAT 599  
 QY 494 GluGlnMetPheGluGlnAsnCysMetGluSerMetGlnAsnTyrProSerThrArg 513  
 Db 600 GAAACAGCTTTGAAGAAAGATGATGAGAGTGGCACTGTAATCGCCTTCAAGTAC 659  
 QY 514 SerProSerLeuSerSerHisProGlyLeuThrThrCysCysSerArgSerIys 533  
 Db 660 ACCCCCTCCCTCTCTCCCAACAGAGACTCNAACAGACTTCTGTCACGAGACACAAA 719  
 QY 534 Lys 534  
 Db 720 AAA 722

RESULT 19  
 CN220459 753 bp mRNA linear EST 08-APR-2004  
 LOCUS RJA06409.ab1 RUBrain Gallus gallus cDNA 5', mRNA sequence.  
 DEFINITION CN220459  
 ACCESSION CN220459  
 VERSION CN220459.1 GI:46299801  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 753)  
 REFERENCE Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and  
 Lundberg, U.  
 EST analysis of brain and testis cDNA libraries from White Leghorn  
 and Red Jungle Fowl  
 Unpublished (2004)  
 CONTACT: Peter Savolainen  
 Department of Biotechnology  
 Royal Institute of Technology, KTH  
 SE-106 91 Stockholm, SWEDEN  
 Tel: +46 (0)8 5537 8481  
 Fax: +46 (0)8 5537 8335  
 Email: Peter.Savolainen@biotech.kth.se  
 Seq primer: M13 reverse primer.  
 Location/Qualifiers

## FEATURES

source

1. .753  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Red junglefowl"  
/db\_xref="taxon:9031"  
/sex="Female"  
/lab\_host="Electromax DH10B (Invitrogen)"  
/clone\_lib="RbBrain"  
/note="Organ: brain; Vector: pSPORT-1; Site\_1: Hind III;  
Site\_2: EcoRI; The cDNA libraries were created with the  
Superscript Plasmid System (Invitrogen)."

ORIGIN

Alignment Scores:

Pred. No.:	8.13e-83	Length:	753
Score:	988.50	Matches:	211
Percent Similarity:	93.70%	Conservative:	12
Best Local Similarity:	88.66%	Mismatches:	14
Query Match:	29.77%	Indels:	6
DB:	7	Gaps:	1

US-10-062-879-4 (1-636) x CN220459 (1-753)

QY 378 Ileaaglylysiilepheyserilecysserleuserglyvalleuvallealeu 397  
::: |||||  
DB 31 GTGACAGGAGATCTTGGCTCATCTGCTGCGAGCGGGCTGCTGATCGCCCTG 90  
QY 398 ProvalProvalilevaliseraspheserargiletyrhiegnasglnarglaasp 417  
91 CCGGTCCTCCGCTCTCCCACTTCAGCGGCATCTACACAGAACCAAGCTCCGAC 150  
QY 418 lyaargatrgalaglnlylevalaargleuvalaargileargvalalalythrglyser 437  
151 AAGGCGGAGACAGAAAGAGCTGCGCTGAGAGATCCGCTGCGCAAGACAGGCGC 210  
QY 438 Serasnalatyrleuhsierlyeargasnlyleuauanglualaleugluleuthr 457  
211 TCCATGCTACCTGCGACAGCAAGCAAGCGCTGCGAAGCAAGCCCTGAGCTGACG 270  
QY 458 Gly---Thrprogluglughisemeglylythrthrserleuilegluserglnhis 476  
|||::: |||||  
DB 271 GATATCCACTGAAGTAAACACATACGACTAAAGCACTCTTATTAAGCAACCAT 330  
QY 477 Histisleuenuhsieyleugluleuthrthrashnhsieglupheillaapgluglnmet 496  
331 CACCACTGCTGCACTGCTG3AAAAAACAACAACAGATTCAATGATGAGCACTG 390  
QY 497 PhegluglnaenCysmetglusersermetglnaenlyrproserthrargserproser 516  
391 TTCAGACGAACTGATGAGAGCTCAATGCAAACTACCCGCTCTTCGAGACCCCTCC 450  
QY 517 LeuserserhisproglyleuthrthrthrCysCysSerargargserlyalythrthr 536  
451 TTGTCAAGTACCAACGGGCTGACCACTCTGCTGTCT-CCGCCGTCACAAGAACCCACG 509  
QY 537 HistleuproanuseraenleuProalathrargleuargsermetglnleuuserthr 556  
510 CACCTTCCCACTCAGGCTGACAGCTACCCGCCCTCCACAGATCAGAACTCAGCACC 569  
QY 557 Ilesisileglnlysergluglnproserleuthrthrserargserleuasnleu 576  
570 ATTCATCCAGTGCAGTGAAGACCCCTCACTTACACCAAGTCTTCCAGTCTACACATG 629  
QY 577 LysalaaparpaglyleuargproasnCysalythrserglnleuthrthralallele 596  
630 AAATCAGATGATGGGCTCGAACCGAACTGCAA-ACCGCCAAATTAACACAGCCATCATC 688  
QY 597 Serleprothrproproalaleuthrprogluglyuserargpropropro 614  
689 AG-ATTCTCG-CCGCGGCGCTCACACCAAGAGT-GAGAGCAAGATCTCCGCA 739

LOCUS AL120075 695 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFPZP761M132.r1.761 (synonym: hamy2) Homo sapiens cDNA clone  
DKFPZP761M132.5', mRNA sequence.  
ACCESSION AL120075  
VERSION AL120075.1 GI:5925974  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 695)  
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and  
Wiemann,S.  
EST (Ottewaelder, et al.)  
JOURNAL Unpublished (1999)  
AUTHORS CONTACT: MIPS  
COMMENT MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Sequenced by Medigenomix (Martinried/Germany) within the cDNA  
sequencing consortium of the German Genome Project. No si sequence  
available.  
This clone (DKFPZP761M132) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heuberweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de.

FEATURES  
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ORIGIN

Alignment Scores:

Pred. No.:	7.99e-83	Length:	695
Score:	988.00	Matches:	193
Percent Similarity:	92.07%	Conservative:	16
Best Local Similarity:	85.02%	Mismatches:	2
Query Match:	29.76%	Indels:	1
DB:	1	Gaps:	1

US-10-062-879-4 (1-636) x AL120075 (1-695)

QY 204 ThrValProCys-----GlyThrValProGlyserlysgluleuProCysGlyGluarg 221  
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DB 2 ACATATCCATATCCCGGCTGTCAGCAGAGCTCTCAAGGAGGAGCCCTGTGGGAAGC 61  
QY 222 TyrservalAlaPhePheCysleuaspThrAlaCysValMetilePheThrValGluTyr 241  
62 TTCCACAGGCGCTTTTGTGATGACACACACCTGTGTACTCATATTCACAGGTGAATAC 121  
DB 242 LeuleuargleuPheAlaAlaProSerArgTyrArgPheileargSerValMetSerile 261  
122 CTCCTGGGGCGTGTGGCGGCGCCAGCGGTTGCGGCTTCCGCGAGTGTATAGGCTTC 181  
QY 262 IleaspValValAlaIleMetProTyrTyrIleGlyLeuValMetThrAsnArgGluasp 281  
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DB 282 ValserGlyAlaPheValThrLeuArgValPheArgValPheArgIlePheIlePheSer 301  
242 GTCTCTGGCGCTTTGTACACCTCGGTGTCTCGGGGTGTTTGCATCTTCAATTCTCC 301  
QY 302 ArgHisserGlnGlyLeuArgIleLeuGlyTyrThrLeuIleuSerCysAlaSerGluLeu 321  
302 AGGCATTCACAGGCGCTTGAGGATTTCTGGGCTACACACTCAAGAGCTGTGCTGAGCTG 361

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